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OM protein - protein search, using sw model

Run on: August 4, 2005, 08:37:33 ; Search time 78.7907 Seconds
(without alignments)
68.722 Million cell updates/sec

Title: US-10-706-275-1

Perfect score: 64

Sequence: 1 ASREAKQVEKALE 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	20	2 AAR43343	Aar43343 B cell ep
2	64	100.0	20	2 AAR97390	Aar97390 Streptoco
3	64	100.0	20	2 AAW69281	Aaw69281 Streptoco
4	64	100.0	29	8 ADK00565	Adk00565 Immunogen
5	64	100.0	45	8 ADK00571	Adk00571 Immunogen
6	64	100.0	46	8 ADK00569	Adk00569 Immunogen
7	64	100.0	46	8 ADK00572	Adk00572 Immunogen
8	64	100.0	47	8 ADK00570	Adk00570 Immunogen
9	64	100.0	234	2 AAR10221	Aar10221 Streptoco
10	64	100.0	236	3 AAR03118	Aar03118 C-terminu
11	64	100.0	254	2 AAR50228	Aar50228 Sequence
12	64	100.0	281	2 AAR20128	Aar20128 Sequence
13	64	100.0	284	2 AAR50229	Aar50229 Sequence
14	64	100.0	305	3 AAR50996	Aar50996 Recombina
15	64	100.0	305	3 AAR03117	Aar03117 S. pyogen
16	64	100.0	441	1 AAP90955	Aap90955 M6 strept
17	64	100.0	441	2 AAR41780	Aar41780 Streptoco
18	64	100.0	441	7 ADG62862	Adg62862 Streptoco
19	64	100.0	483	2 AAW08927	Aaw08927 Type-6 M-
20	64	100.0	484	5 ABR30015	Abp30015 Streptoco
21	64	100.0	484	8 ADR83969	Adr83969 S. pyogen
22	64	100.0	539	8 ADP43327	Adp43327 S. pyogen
23	57	89.1	28	2 AAW04353	Aaw04353 Chimaeric
24	56	87.5	12	2 AAR97415	Aar97415 Streptoco
25	56	87.5	28	2 AAW04354	Aaw04354 Chimaeric

26	56	87.5	28	2 AAW04355	Aaw04355 Chimaeric
27	55	85.9	12	2 AAR97413	Aar97413 Streptoco
28	55	85.9	12	2 AAR97414	Aar97414 Streptoco
29	53	82.8	22	7 ADG62865	Adg62865 Streptoco
30	53	82.8	65	7 ADG62863	Adg62863 Streptoco
31	52	81.2	28	2 AAW04352	Aaw04352 Chimaeric
32	51	79.7	12	2 AAR97412	Aar97412 Streptoco
33	48	75.0	21	7 ADG62867	Adg62867 Streptoco
34	47.5	74.2	28	2 AAW04351	Aaw04351 Chimaeric
35	46	71.9	12	2 AAR97411	Aar97411 Streptoco
36	46	71.9	20	2 AAR97426	Aar97426 Streptoco
37	45	70.3	546	8 ADN22689	Adn22689 Bacterial
38	44.5	69.5	28	2 AAW04350	Aaw04350 Chimaeric
39	44	68.8	153	6 ABP80572	Abp80572 N. gonorr
40	44	68.8	153	6 ABP80951	Abp80951 N. gonorr
41	44	68.8	206	3 AAY74875	Aay74875 Neisseria
42	44	68.8	277	3 AAY74876	Aay74876 Neisseria
43	43	67.2	94	3 AAB03122	Aab03122 Streptoco
44	43	67.2	343	2 AAR50999	Aar50999 Recombina
45	43	67.2	343	3 AAB03121	Aab03121 S. pyogen

ALIGNMENTS

RESULT 1

AAR43343
ID AAR43343 standard; peptide; 20 AA.

AC AAR43343;

XX 25-MAR-2003 (revised)

DT 21-MAY-1994 (first entry)

XX B cell epitope from Streptococcus M protein.

XX Group A beta haemolytic streptococci; antibody; human heart tissue;
KW vaccine; humoral immunity; diagnosis.

XX Synthetic.

XX W09321220-A1.

XX 28-OCT-1993.

XX 30-MAR-1993; 93WO-AU000131.

XX 08-APR-1992; 92AU-00001800.

XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.

XX Good MF, Pruksakorn S;

XX WPI; 1993-351655/44.

XX Synthetic peptide - comprises at least one B-cell epitope from
PT streptococcal M-protein, useful in vaccine for streptococcal infections.

XX Claim 7; Page 38; 57pp; English.

XX The peptide comprises an N-terminal sequence derived from the conserved
CC region of the M protein of group A beta-haemolytic streptococci (residues
337-492 of the type 5 M-protein). The peptide shown, peptide 145
CC comprises at least 1 B cell epitope, where an antibody reactive to the B
CC cell epitope is only minimally reactive to human heart tissue. The
CC peptide is useful in a vaccine for inducing humoral immunity against
CC streptococcal infections. Antibodies to the peptide are useful in
CC diagnosis of such infections. (Updated on 25-MAR-2003 to correct PN
field.)

XX Sequence 20 AA;

XX Query Match

100.0%; Score 64; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.0019; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
|||||

Db 7 ASREAKKQVEKALE 20

RESULT 2
AAR97390
ID AAR97390 standard; peptide; 20 AA.
XX
AC AAR97390;
XX
XX 27-AUG-2003 (revised)
DT 02-DEC-1996 (first entry)
XX
XX Streptococcal M protein peptide p145, for use in chimaeric peptide.
XX
XX Streptococcal; M protein; peptide; p145; chimaeric; chimeric; B-cell;
KW conformational epitope; alpha-helix; GCN4; leucine zipper; detection;
KW mapping; opsonic antibody; vaccine; group A Streptococci; immunotherapy;
KW diagnosis.
XX
OS Streptococcus sp.
XX
XX WO9611944-A1.
PN
XX
XX 25-APR-1996.
PD
XX
XX 16-OCT-1995; 95WO-AU000681.
PF
XX
XX 14-OCT-1994; 94AU-00008851.
PR
XX
XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (UYME) UNIV MELBOURNE.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.
PA (CSLC-) CSL LTD.
XX
XX Cooper JA, Relf WA, Good MF, Saul AJ;
PI
XX WPI; 1996-221939/22.
DR
XX
XX New chimeric peptide(s) including a conformational epitope - inserted
PT into a peptide having similar native conformation, useful in vaccines and
PT for determin. of minimal epitope(s) or for mapping amphipathic helices.
XX
XX
XX Claim 4; Page 80; 99pp; English.
PS
XX
XX The present peptide is the Streptococcal M protein peptide p145
CC (Pruksakorn et al, J. Immunol. 149: 2729-2735 (1992)), used in the
CC construction of a novel chimeric peptide (CP). The CP comprises a B-cell
CC conformational epitope from within the present peptide, inserted into a
CC 2nd peptide, pref. an alpha-helical coil based on the GCN4 leucine zipper
CC peptide (AAR97395). The 2nd peptide has a similar conformation, enabling
CC the epitope to be presented in an immunologically active conformation.
CC The CP can be used in a novel detection/mapping process, e.g. to
CC determine the min. epitope required to induce opsonic antibodies (Ab),
CC and in vaccines against sp. A Streptococci. Ab raised against the CP can
CC be used for immunotherapy and diagnosis, while the CP can be used
CC diagnostically to detect Ab. (Updated on 27-AUG-2003 to correct OS
CC field.)
XX
XX Sequence 20 AA;

Query Match 100.0%; Score 64; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
|||||

Db 7 ASREAKKQVEKALE 20

RESULT 3
AAW69281
ID AAW69281 standard; peptide; 20 AA.
XX
XX AAW69281;
AC
XX
XX 29-OCT-1998 (first entry)
DT
XX
XX Streptococcus group A protein fragment.
DE
XX
XX Acryloylated peptide polymer; immune response; peptide epitope;
KW synthetic vaccine; enzymatically cleavable site.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 1
FT /note= "linked to acryloylated peptide polymer"
XX
XX WO9834968-A1.
PN
XX
XX 13-AUG-1998.
PD
XX
XX 10-FEB-1998; 98WO-AU0000076.
PF
XX
XX 11-FEB-1997; 97AU-00005071.
PR
XX 03-OCT-1997; 97CA-02217321.
XX
XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (UYME) UNIV MELBOURNE.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PA (CSLC-) CSL LTD.
XX
XX Jackson DC, O'Brien-Simpson NM, Brown LE, Zeng W, Ede NJ;
PI Brandt ER, Good MF;
PI
XX WPI; 1998-447177/38.
DR
XX
XX Acryloylated peptide polymers - useful for synthetic vaccine technology,
PT for raising an immune response to peptide epitope and as diagnostic tool.
PT
XX
XX Example 1; Page 20; 77pp; English.
PS
XX
XX This sequence represents a fragment of a Streptococcus group A protein.
CC This sequence was used to test the acryloylated peptide polymer of the
CC invention. The peptide polymers are used to raise an immune response to a
CC peptide epitope (such as this sequence), and also as diagnostic tools.
CC Polymers (molecular wt. >600 kDa.) can be prepared with virtually any
CC number of the same or different epitopes by a method that allows
CC purification of the individual determinants, avoids errors inherent in
CC long sequential syntheses in which protected peptide fragments are not
CC used, thus avoiding solubility and purification problems. Multiple copies
CC of many different peptide epitopes may be incorporated into a single
CC polymeric structure to allow utilization of the range of T cell epitopes
CC required for outbred populations in conjunction with epitopes
CC representing different pathogenic serotypes, thus making them a
CC significant advance in synthetic vaccine technology
XX
XX Sequence 20 AA;

Query Match 100.0%; Score 64; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
|||||

Db 7 ASREAKKQVEKALE 20

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RESULT 4
ADK00565
ID ADK00565 standard; peptide; 29 AA.
XX
AC ADK00565;
XX
DT 06-MAY-2004 (first entry)
XX
DE Immunogenic lipopeptide of the invention #101.
XX
KW T helper cell epitope; B cell epitope; Antibacterial; Antiulcer;
KW Antiinfertility; Vaccine; antibody.
XX
OS Synthetic.
XX
PN WO2004014956-A1.
XX
PD 19-FEB-2004.
XX
PF 12-AUG-2003; 2003WO-AU001018.
XX
PR 12-AUG-2002; 2002US-0402838P.
XX
PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
XX
PI Jackson D, Zeng W;
XX
DR WPI; 2004-238735/22.
XX
PT Novel lipopeptide comprising polypeptide having amino acid sequence of T
PT helper cell epitope and B cell epitope, conjugated to lipid moieties,
PT useful for eliciting immune response against group A Streptococcus
PT antigen.
XX
PS Claim 29; SEQ ID NO 101; 194pp; English.
XX
CC The present invention relates to a lipopeptide comprising polypeptide
CC conjugated to lipid moieties, where polypeptide contains amino acid
CC sequence of T helper cell epitope and B cell epitope, where amino acid
CC sequences are different, and internal lysine residues or internal lysine
CC analog residues for covalent attachment of each of lipid moieties through
CC <math>\epsilon</math>-amino group or terminal side chain group of lysine or lysine
CC analog. The peptides are useful in eliciting the production of antibody
CC against an antigenic B cell epitope in a subject, and are useful for
CC antibody production, synthetic vaccine production, diagnostic method
CC employing antibodies and antibody ligands and immunotherapy for
CC veterinary and human medicine. The method efficiently elicits the
CC production of antibody against antigenic B cell epitope. The present
CC sequence represents a novel immunogenic lipopeptide comprising T helper
CC and B cell epitopes.
XX
SQ Sequence 29 AA;
Query Match 100.0%; Score 64; DB 8; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASREAKKQVEKALE 14
Db 9 ASREAKKQVEKALE 22
RESULT 5
ADK00571
ID ADK00571 standard; peptide; 45 AA.
XX
AC ADK00571;
XX
DT 06-MAY-2004 (first entry)
XX
DE Immunogenic lipopeptide of the invention #107.
XX
KW T helper cell epitope; B cell epitope; Antibacterial; Antiulcer;

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KW Antiinfertility; Vaccine; antibody.
XX
OS Synthetic.
XX
PN WO2004014956-A1.
XX
PD 19-FEB-2004.
XX
PF 12-AUG-2003; 2003WO-AU001018.
XX
PR 12-AUG-2002; 2002US-0402838P.
XX
PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
XX
PI Jackson D, Zeng W;
XX
DR WPI; 2004-238735/22.
XX
PT Novel lipopeptide comprising polypeptide having amino acid sequence of T
PT helper cell epitope and B cell epitope, conjugated to lipid moieties,
PT useful for eliciting immune response against group A Streptococcus
PT antigen.
XX
PS Claim 39; SEQ ID NO 107; 194pp; English.
XX
CC The present invention relates to a lipopeptide comprising polypeptide
CC conjugated to lipid moieties, where polypeptide contains amino acid
CC sequence of T helper cell epitope and B cell epitope, where amino acid
CC sequences are different, and internal lysine residues or internal lysine
CC analog residues for covalent attachment of each of lipid moieties through
CC <math>\epsilon</math>-amino group or terminal side chain group of lysine or lysine
CC analog. The peptides are useful in eliciting the production of antibody
CC against an antigenic B cell epitope in a subject, and are useful for
CC antibody production, synthetic vaccine production, diagnostic method
CC employing antibodies and antibody ligands and immunotherapy for
CC veterinary and human medicine. The method efficiently elicits the
CC production of antibody against antigenic B cell epitope. The present
CC sequence represents a novel immunogenic lipopeptide comprising T helper
CC and B cell epitopes.
XX
SQ Sequence 45 AA;
Query Match 100.0%; Score 64; DB 8; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASREAKKQVEKALE 14
Db 25 ASREAKKQVEKALE 38
RESULT 6
ADK00569
ID ADK00569 standard; peptide; 46 AA.
XX
AC ADK00569;
XX
DT 06-MAY-2004 (first entry)
XX
DE Immunogenic lipopeptide of the invention #105.
XX
KW T helper cell epitope; B cell epitope; Antibacterial; Antiulcer;
KW Antiinfertility; Vaccine; antibody.
XX
OS Synthetic.
XX
PN WO2004014956-A1.
XX
PD 19-FEB-2004.
XX
PF 12-AUG-2003; 2003WO-AU001018.
XX
PR 12-AUG-2002; 2002US-0402838P.

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XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 XX PI Jackson D, Zeng W;
 XX DR WPI; 2004-238735/22.
 XX PT Novel lipopeptide comprising polypeptide having amino acid sequence of T
 PT helper cell epitope and B cell epitope, conjugated to lipid moieties,
 PT useful for eliciting immune response against group A Streptococcus
 PT antigen.
 XX PS Claim 39; SEQ ID NO 105; 194pp; English.
 XX CC The present invention relates to a lipopeptide comprising polypeptide
 CC conjugated to lipid moieties, where polypeptide contains amino acid
 CC sequence of T helper cell epitope and B cell epitope, where amino acid
 CC sequences are different, and internal lysine residues or internal lysine
 CC analog residues for covalent attachment of each of lipid moieties through
 CC segr; amino group or terminal side chain group of lysine or lysine
 CC against an antigenic B cell epitope in a subject, and are useful for
 CC antibody production, synthetic vaccine production, diagnostic method
 CC employing antibodies and antibody ligands and immunotherapy for
 CC veterinary and human medicine. The method efficiently elicits the
 CC production of antibody against antigenic B cell epitope. The present
 CC sequence represents a novel immunogenic lipopeptide comprising T helper
 CC and B cell epitopes.
 XX SQ Sequence 46 AA;
 Query Match 100.0%; Score 64; DB 8; Length 46;
 Best Local Similarity 100.0%; Pred. No. 0.0047;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ASREAKKQVEKALE 14
 |||||
 26 ASREAKKQVEKALE 39
 Db
 RESULT 7
 ADK00572
 ID ADK00572 standard; peptide; 46 AA.
 XX AC
 AC ADK00572;
 XX DT 06-MAY-2004 (first entry)
 XX DE Immunogenic lipopeptide of the invention #108.
 XX KW T helper cell epitope; B cell epitope; Antibacterial; Antiulcer;
 KW Antiinfertility; Vaccine; antibody.
 XX OS Synthetic.
 XX PN WO2004014956-A1.
 XX PD 19-FEB-2004.
 XX PF 12-AUG-2003; 2003WO-AU001018.
 XX PR 12-AUG-2002; 2002US-0402838P.
 XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 XX PI Jackson D, Zeng W;
 XX DR WPI; 2004-238735/22.
 XX PT Novel lipopeptide comprising polypeptide having amino acid sequence of T
 PT helper cell epitope and B cell epitope, conjugated to lipid moieties,
 PT useful for eliciting immune response against group A Streptococcus
 PT antigen.

XX PS Claim 39; SEQ ID NO 108; 194pp; English.
 XX CC The present invention relates to a lipopeptide comprising polypeptide
 CC conjugated to lipid moieties, where polypeptide contains amino acid
 CC sequence of T helper cell epitope and B cell epitope, where amino acid
 CC sequences are different, and internal lysine residues or internal lysine
 CC analog residues for covalent attachment of each of lipid moieties through
 CC segr; amino group or terminal side chain group of lysine or lysine
 CC against an antigenic B cell epitope in a subject, and are useful for
 CC antibody production, synthetic vaccine production, diagnostic method
 CC employing antibodies and antibody ligands and immunotherapy for
 CC veterinary and human medicine. The method efficiently elicits the
 CC production of antibody against antigenic B cell epitope. The present
 CC sequence represents a novel immunogenic lipopeptide comprising T helper
 CC and B cell epitopes.
 XX SQ Sequence 46 AA;
 Query Match 100.0%; Score 64; DB 8; Length 46;
 Best Local Similarity 100.0%; Pred. No. 0.0047;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ASREAKKQVEKALE 14
 |||||
 26 ASREAKKQVEKALE 39
 Db
 RESULT 8
 ADK00570
 ID ADK00570 standard; peptide; 47 AA.
 XX AC
 AC ADK00570;
 XX DT 06-MAY-2004 (first entry)
 XX DE Immunogenic lipopeptide of the invention #106.
 XX KW T helper cell epitope; B cell epitope; Antibacterial; Antiulcer;
 KW Antiinfertility; Vaccine; antibody.
 XX OS Synthetic.
 XX PN WO2004014956-A1.
 XX PD 19-FEB-2004.
 XX PF 12-AUG-2003; 2003WO-AU001018.
 XX PR 12-AUG-2002; 2002US-0402838P.
 XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 XX PI Jackson D, Zeng W;
 XX DR WPI; 2004-238735/22.
 XX PT Novel lipopeptide comprising polypeptide having amino acid sequence of T
 PT helper cell epitope and B cell epitope, conjugated to lipid moieties,
 PT useful for eliciting immune response against group A Streptococcus
 PT antigen.
 XX PS Claim 39; SEQ ID NO 106; 194pp; English.
 XX CC The present invention relates to a lipopeptide comprising polypeptide
 CC conjugated to lipid moieties, where polypeptide contains amino acid
 CC sequence of T helper cell epitope and B cell epitope, where amino acid
 CC sequences are different, and internal lysine residues or internal lysine
 CC analog residues for covalent attachment of each of lipid moieties through
 CC segr; amino group or terminal side chain group of lysine or lysine
 CC against an antigenic B cell epitope in a subject, and are useful for
 CC antibody production, synthetic vaccine production, diagnostic method
 CC employing antibodies and antibody ligands and immunotherapy for
 CC veterinary and human medicine. The method efficiently elicits the
 CC production of antibody against antigenic B cell epitope. The present
 CC sequence represents a novel immunogenic lipopeptide comprising T helper
 CC and B cell epitopes.

CC antibody production, synthetic vaccine production, diagnostic method
 CC employing antibodies and antibody ligands and immunotherapy for
 CC veterinary and human medicine. The method efficiently elicits the
 CC production of antibody against antigenic B cell epitope. The present
 CC sequence represents a novel immunogenic lipopeptide comprising T helper
 CC and B cell epitopes.

XX SQ Sequence 47 AA;

Query Match 100.0%; Score 64; DB 8; Length 47;
 Best Local Similarity 100.0%; Pred. No. 0.0048;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ASREAKKQVEKALE 14
 |||||
 Db 27 ASREAKKQVEKALE 40

RESULT 9
 AAR10221
 ID AAR10221 standard; protein; 234 AA.

XX AC AAR10221;

DT 25-MAR-2003 (revised)
 DT 26-MAR-1991 (first entry)

XX DE Streptococcal M6' protein.

XX KW Streptococcal M protein; M'6 protein; vaccinia virus; fowlpox virus;
 XX KW poxviridae vaccine; streptococcal pharyngitis.

XX OS Streptococcus sp.

XX PN WO9015872-A.

XX PD 27-DEC-1990.

XX PF 21-JUN-1989; 89US-00369118.

XX PR 21-JUN-1989; 89US-00369118.

XX BR 19-JUN-1990; 90US-00540586.

XX PA (UYRQ) UNIV ROCKEFELLER.

XX PA (UYOR-) UNIV OREGON STATE.

XX PI Fischetti VA, Kruby DE;

XX XX WPI; 1991-022236/03.

XX DR N-PSDB; AAQ10244.

XX PT New recombinant streptococcal M protein DNA and viral vector - for
 XX PT production of poxviridae vaccines in treatment of vaccinia, fowlpox etc.

XX PS Disclosure; Fig 5; 4lpp; English.

XX CC This M'6 protein corresponds to the conserved exposed polypeptide region
 CC of the streptococcal M protein. It is encoded by a gene- tically
 CC engineered gene introduced into the genome of a vaccinia or fowlpox
 CC virus. The resultant DNA complex is useful as a vaccine for
 CC immunoprotection against streptococcal infections. The M'6 polypeptide is
 CC the part of protein M responsible for virulence. (Updated on 25-MAR-2003
 CC to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 234 AA;

Query Match 100.0%; Score 64; DB 2; Length 234;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ASREAKKQVEKALE 14
 |||||
 Db 85 ASREAKKQVEKALE 98

RESULT 10
 AAB03118

ID AAB03118 standard; protein; 236 AA.

XX AC AAB03118;

XX DT 10-OCT-2000 (first entry)

XX DE C-terminus of Streptococcus pyogenes M protein M5.

XX KW Multivalent hybrid M protein; M5; group A streptococcus; serotype;
 XX KW immunogenic; sero-specific antibody; streptococcal infection;
 XX KW cross reactivity; vaccine; acute rheumatic fever; ARF;
 XX KW rheumatic heart disease; streptococcal pharyngitis; strep throat;
 XX KW pneumonia.

XX OS Streptococcus pyogenes.

XX PN US6063386-A.

XX PD 16-MAY-2000.

XX PF 15-SEP-1997; 97US-00937271.

XX PR 16-SEP-1992; 92US-00945954.

XX PA (UYTE-) UNIV TENNESSEE RES CORP.

XX PI Lederer JW, Dale JB;

XX XX WPI; 2000-364475/31.

XX PT New immunogenic recombinant hybrid M protein comprising amino-terminal
 XX PT peptide fragments of streptococcal M protein useful as vaccine against
 XX PT rheumatic fever and infections leading to rheumatic fever.

XX PS Disclosure; Col 45-46; 62pp; English.

XX CC The invention relates to multivalent immunogenic hybrid group A
 CC streptococcal M proteins comprising N-terminal peptide fragments of M
 CC proteins that elicit opsonic antibodies against multiple serotypes of
 CC group A streptococci (e.g., Streptococcus pyogenes). The antibodies
 CC generated using the hybrid proteins are against one or more M protein
 CC serotypes, where at least one of the serotypes is M1, M3, M18 or M19. The
 CC invention also encompasses a recombinant DNA molecule comprising a
 CC nucleotide sequence that encodes a multivalent hybrid M protein; and a
 CC method for immunising a mammal against streptococcal infections,
 CC comprising administering an immunogenic multivalent hybrid M protein to
 CC the mammal. The multivalent hybrid M proteins are useful for eliciting
 CC opsonic or protective antibodies to the M proteins of different serotypes
 CC of group A streptococci, and may therefore be used as vaccines to protect
 CC against and control infection by type A streptococci. Type A streptococci
 CC are not only responsible for streptococcal pharyngitis (strep throat),
 CC forms of pneumonia and a condition resembling toxic shock, but are also
 CC involved in the development of acute rheumatic fever (ARF) and rheumatic
 CC heart disease. In a patient with ARF, antibodies formed during a group A
 CC streptococcal infection are also cross-reactive with heart tissue, which
 CC indicates that the streptococci and host tissue contain similar antigenic
 CC motifs. The new multivalent vaccines are capable of raising sero-specific
 CC antibodies against various serotypes of group A streptococci which are
 CC not cross-reactive with human heart tissue. The present sequence
 CC represents the C-terminal half of the Streptococcus pyogenes M5 protein,
 CC which is a component of the tetraivalent M24-M5-M6-M19 hybrid M protein
 CC AAB03117

XX SQ Sequence 236 AA;

Query Match 100.0%; Score 64; DB 3; Length 236;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
 DB 87 ASREAKKQVEKALE 100

RESULT 11
 AAR50228
 ID AAR50228 standard; protein; 254 AA.
 AC
 XX AAR50228;
 XX
 DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 09-OCT-1994 (first entry)
 XX
 DE Sequence of a fragment of Group A streptococcal surface protein M5 and a
 DE carrier of the COOH-terminal portion of M5.
 XX
 KW B subunit; labile toxin; M protein; fusion protein; antigen;
 KW Group A streptococci; rheumatic fever; pharyngitis.
 XX
 OS Streptococcus sp.
 XX WO9406465-A1.
 PN
 XX 31-MAR-1994.
 PD
 XX 15-SEP-1993; 93WO-US008704.
 PF
 XX 16-SEP-1992; 92US-00945860.
 PR
 XX (UYTE-) UNIV TENNESSEE RES CORP.
 PA
 XX Dale JB;
 PI
 XX WPI; 1994-118162/14.
 DR N-PSDB; AAQ45160.
 XX
 PT New recombinant hybrid streptococcal M protein antigen(s) - which elicit
 PT opsonic antibodies without eliciting cross-reactive antibodies to
 PT mammalian heart tissue.
 XX
 PS Disclosure; Fig 4; 45pp; English.
 XX
 CC The surface M protein of Group A streptococci is the major virulence
 CC factor and protective antigen of these organisms. However, there are a
 CC tremendous number of M protein serotypes. The invention provides
 CC recombinant M protein antigens comprising a gene encoding a carrier
 CC protein and an NH2 or COOH terminal M protein fragment carrying one or
 CC more epitopes. The carrier may be the B subunit of E.coli labile toxin
 CC (LT-B) or the C-repeat portion of a streptococcal M protein. For example,
 CC AAQ45160/R50228 comprises an antigen which is an M5 hapten fragment of 16
 CC AAs joined by a BamHI restriction site to a carrier which is the COOH-
 CC terminal half of M5. The carrier includes 2.5 C-repeats, which each
 CC commence with the tetrapeptide NKIS. A linker could be inserted at the
 CC BamHI site. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-
 CC AUG-2003 to correct OS field.)
 XX
 SQ Sequence 254 AA;
 Query Match 100.0%; Score 64; DB 2; Length 254;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
 DB 105 ASREAKKQVEKALE 118

RESULT 12
 AAR20128
 ID AAR20128 standard; protein; 281 AA.
 XX

AC AAR20128;
 XX
 DT 27-AUG-2003 (revised)
 DT 15-APR-1992 (first entry)
 XX
 DE Sequence encoded by truncated M1 gene.
 XX
 KW Protein H; immunoglobulin G; IgG; antibody; autoimmune disease.
 XX
 OS Streptococcus sp.
 XX
 XX Key Location/Qualifiers
 FH Region 1..28
 FT /label= p16W1
 FT Region 29..70
 FT /label= C1
 FT Region 71..112
 FT /label= C2
 FT Region 113..155
 FT /label= C3
 FT Region 156..176
 FT /label= C4
 FT Region 177..281
 FT /label= D
 XX
 PN WO9119740-A.
 XX
 XX 26-DEC-1991.
 PD
 XX 21-JUN-1990; 90SE-00002212.
 PF
 XX 21-JUN-1990; 90SE-00002212.
 PR
 XX (HIGH-) HIGHTECH RECEPTOR A.
 PA
 XX Schmidt KH, Akesson P, Cooney J, Bjorck L;
 PI WPI; 1992-024366/03.
 XX N-PSDB; AAQ20292.
 DR
 XX New IgG binding proteins H' lacking an albumin binding sequence - useful
 PT in purificn. of excess IgG from blood and to diagnose autoimmune
 PT diseases.
 XX
 PS Disclosure; Fig 8; 37pp; English.
 CC The inventors claim a protein prod. by a strain of Gp.A Streptococci. The
 CC protein has the AA sequence of protein H but lacks at least some part of
 CC the C and D regions (responsible for binding albumin), esp. it lacks the
 CC whole of these regions and extends for AAl to AAl58. Compared with
 CC natural protein H, it is more specific and may be used as part of a kit
 CC for the binding, separation and identification of human IgG. The same
 CC sequences appear in WO9119741. (Updated on 27-AUG-2003 to correct OS
 CC field.)
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 64; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
 DB 132 ASREAKKQVEKALE 145

RESULT 13
 AAR50229
 ID AAR50229 standard; protein; 284 AA.
 XX
 AC AAR50229;
 XX
 DT 27-AUG-2003 (revised)

```

DT 25-MAR-2003 (revised)
XX 09-OCT-1994 (first entry)
DE Sequence of fragments of Group A streptococcal surface protein M5 and a
DE carrier of the COOH-terminal portion of M5.
XX
XX B subunit; labile toxin; M protein; fusion protein; antigen;
XX Group A streptococci; rheumatic fever; pharyngitis.
XX
XX Streptococcus sp.
XX
XX WO9406465-A1.
XX
XX 31-MAR-1994.
XX
XX 15-SEP-1993; 93WO-US008704.
XX
XX 16-SEP-1992; 92US-00945860.
XX
XX (UYTE-) UNIV TENNESSEE RES CORP.
XX
XX Dale JB;
XX
XX WPI; 1994-118162/14.
XX N-PSDB; AAQ45161.
XX
XX New recombinant hybrid streptococcal M protein antigen(s) - which elicit
XX opsonic antibodies without eliciting cross-reactive antibodies to
XX mammalian heart tissue.
XX
XX Disclosure; Fig 5; 45pp; English.
XX
XX The surface M protein of Group A streptococci is the major virulence
XX factor and protective antigen of these organisms. However, there are a
XX tremendous number of M protein serotypes. The invention provides
XX recombinant M protein antigens comprising a gene encoding a carrier
XX protein and an NH2 or COOH terminal M protein fragment carrying one or
XX more epitopes. The carrier may be the B subunit of E.coli labile toxin
XX (LT-B) or the C-repeat portion of a streptococcal M protein. For example,
XX AAQ45161/R50229 comprises three segments of M5 designated A,B and C. The
XX C segment is joined by a BamHI restriction site to a carrier which is the
XX COOH-terminal half of M5. The carrier includes 2.5 C-repeats, which each
XX commence with the tetrapeptide NKIS. A linker could be inserted at the
XX BamHI site. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-
XX AUG-2003 to correct OS field.)
XX
XX SQ Sequence 284 AA;
XX
XX Query Match 100.0%; Score 64; DB 2; Length 284;
XX Best Local Similarity 100.0%; Pred. No. 0.032;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ASREAKKQVEKALE 14
XX |||||
XX Db 135 ASREAKKQVEKALE 148
XX
XX RESULT 14
XX AAR50996
XX ID AAR50996 standard; protein; 305 AA.
XX
XX AAR50996;
XX
XX 25-MAR-2003 (revised)
XX 02-NOV-1994 (first entry)
XX
XX Recombinant M24-M5-M6-M19 C-term variant.
XX
XX Primer; PCR; amplify; polymerase chain reaction; construct; hybrid;
XX M protein; M24; M5; M6; M19; subunit; tetraivalent protein; emm gene;
XX tandem; PKX223.3; protective epitope; tissue-cross-reactive epitope;
XX restriction enzyme site; multivalent M protein; immunisation; group A;
XX streptococci; rheumatic fever; rheumatic heart disease; humoral;

```

```

KW antibody; heart tissue; antigen; serotype; mucosal.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..18
XX Peptide /label= M24
XX Peptide 19..35
XX Peptide /label= M5
XX Peptide 36..52
XX Peptide /label= M6
XX Peptide 53..69
XX Peptide /label= M19
XX Peptide 70..305
XX Peptide /label= M5 C-terminal_fragment
XX
XX WO9406421-A1.
XX
XX 31-MAR-1994.
XX
XX 15-SEP-1993; 93WO-US008703.
XX
XX 16-SEP-1992; 92US-00945954.
XX
XX (UYTE-) UNIV TENNESSEE RES CORP.
XX
XX Dale JB, Lederer JW;
XX
XX WPI; 1994-118122/14.
XX N-PSDB; AAQ45218.
XX
XX New immunogenic hybrid proteins derives from streptococcal M proteins -
XX induces opsonic antibodies, for protective immunisation against multiple
XX group A streptococci serotypes.
XX
XX Disclosure; Fig 8; 67pp; English.
XX
XX The sequences given in AAR50992-1001 represent hybrid M proteins which
XX contain the M24-M5-M6 and/or M19 subunits. These multivalent proteins
XX were constructed using fragments of the 5' regions of emm genes that were
XX amplified by PCR, ligated in tandem and expressed in pKX223.3. The
XX amplified regions pref. encode protective and not tissue-cross-reactive
XX epitopes, which can then be linked into one protein molecule. The
XX recombinant hybrid protein may contain 113 N-terminal amino acids of M24,
XX 58 amino acids of M5, 35 from M6 and 35 from M19. Each section is linked
XX by 2 amino acids specified by the respective restriction enzyme sites
XX that were synthesised into the primers used to specify the PCR product.
XX Multivalent M proteins such as this may be used for protective
XX immunisation against group A streptococci, which esp. cause rheumatic
XX fever and rheumatic heart disease. Humoral antibodies raised against
XX these proteins do not react with heart tissue antigens but are effective
XX against many different serotypes. The multivalent proteins may also
XX include sequences which induce mucosal antibodies and do not require
XX coupling to an immunogenic carrier. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX
XX SQ Sequence 305 AA;
XX
XX Query Match 100.0%; Score 64; DB 2; Length 305;
XX Best Local Similarity 100.0%; Pred. No. 0.034;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ASREAKKQVEKALE 14
XX |||||
XX Db 156 ASREAKKQVEKALE 169
XX
XX RESULT 15
XX AAB03117
XX ID AAB03117 standard; protein; 305 AA.
XX
XX AAB03117;
XX

```

Job time : 79.7907 secs

DT 10-OCT-2000 (first entry)
 XX S. pyogenes hybrid M protein (M24-M5-M6-M19) , SEQ ID NO:10.
 XX
 XX Multivalent hybrid M protein; group A streptococcus; serotype;
 KW immunogenic; sero-specific antibody; streptococcal infection;
 KW cross reactivity; vaccine; acute rheumatic fever; ARF;
 KW rheumatic heart disease; streptococcal pharyngitis; strep throat;
 KW pneumonia.
 XX
 XX Streptococcus pyogenes.
 OS Synthetic.
 OS
 XX US6063386-A.
 PN
 XX 16-MAY-2000.
 PD
 XX
 XX 15-SEP-1997; 97US-00937271.
 PF
 XX
 XX 16-SEP-1992; 92US-00945954.
 PR
 XX (UYTE-) UNIV TENNESSEE RES CORP.
 PA
 XX Lederer JW, Dale JB;
 PI
 XX WPI; 2000-364475/31.
 DR
 XX N-PSDB; AAA57897.
 DR
 XX
 XX New immunogenic recombinant hybrid M protein comprising amino-terminal
 PT peptide fragments of streptococcal M protein useful as vaccine against
 PT rheumatic fever and infections leading to rheumatic fever.
 XX
 XX Disclosure; Fig 8A-B; 62pp; English.
 PS
 XX
 XX The invention relates to multivalent immunogenic hybrid group A
 CC streptococcal M proteins comprising N-terminal peptide fragments of M
 CC proteins that elicit opsonic antibodies against multiple serotypes of
 CC group A streptococci (e.g., Streptococcus pyogenes). The antibodies
 CC generated using the hybrid proteins are against one or more M protein
 CC serotypes, where at least one of the serotypes is M1, M3, M18 or M19. The
 CC invention also encompasses a recombinant DNA molecule comprising a
 CC nucleotide sequence that encodes a multivalent hybrid M protein; and a
 CC method for immunising a mammal against streptococcal infections,
 CC comprising administering an immunogenic multivalent hybrid M protein to
 CC the mammal. The multivalent hybrid M proteins are useful for eliciting
 CC opsonic or protective antibodies to the M proteins of different serotypes
 CC of group A streptococci, and may therefore be used as vaccines to protect
 CC against and control infection by type A streptococci. Type A streptococci
 CC are not only responsible for streptococcal pharyngitis (strep throat),
 CC forms of pneumonia and a condition resembling toxic shock, but are also
 CC involved in the development of acute rheumatic fever (ARF) and rheumatic
 CC heart disease. In a patient with ARF, antibodies formed during a group A
 CC streptococcal infection are also cross-reactive with heart tissue, which
 CC indicates that the streptococci and host tissue contain similar antigenic
 CC motifs. The new multivalent vaccines are capable of raising sero-specific
 CC antibodies against various serotypes of group A streptococci which are
 CC not cross-reactive with human heart tissue. Sequences AAB03113-B03117,
 CC AAB03119-B03121 and AAB03123-B03124 represent multivalent hybrid
 CC Streptococcus pyogenes M proteins generated in the disclosure of the
 CC invention
 CC
 XX
 XX Sequence 305 AA;
 SQ
 Query Match 100.0%; Score 64; DB 3; Length 305;
 Best Local Similarity 100.0%; Pred. No. 0.034;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ASREAKKQVEKALE 14
 |||||
 Db 156 ASREAKKQVEKALE 169

Search completed: August 4, 2005, 08:59:23

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2005, 08:27:17 ; Search time 19.5349 Seconds
(without alignments)
53.498 Million cell updates/sec

Title: US-10-706-275-1

Perfect score: 64
Sequence: 1 ASREAKQVEKALE 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
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5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfileei.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	100.0	20	3	US-08-817-811-1
2	64	100.0	236	3	US-08-937-271-11
3	64	100.0	254	4	US-08-914-479A-4
4	64	100.0	284	4	US-08-914-479A-6
5	64	100.0	305	3	US-08-937-271-10
6	64	100.0	440	4	US-08-302-756R-35
7	64	100.0	443	2	US-08-795-475-6
8	64	100.0	443	4	US-08-325-278B-6
9	56	87.5	12	3	US-08-817-811-34
10	55	85.9	12	3	US-08-817-811-11
11	55	85.9	12	3	US-08-817-811-32
12	55	85.9	12	3	US-08-817-811-33
13	52	81.2	28	3	US-08-817-811-18
14	51	79.7	28	3	US-08-817-811-31
15	47.5	74.2	28	3	US-08-817-811-17
16	46	71.9	12	3	US-08-817-811-10
17	46	71.9	12	3	US-08-817-811-30
18	46	71.9	20	3	US-08-817-811-38
19	44.5	69.5	28	3	US-08-817-811-16
20	43	67.2	94	3	US-08-937-271-18
21	43	67.2	343	3	US-08-937-271-17
22	43	67.2	683	6	5210183-3
23	43	67.2	683	6	5210183-3
24	42	65.6	65	1	US-08-464-531-83
25	42	65.6	65	2	US-08-461-598-83
26	42	65.6	65	3	US-08-322-137-83
27	42	65.6	380	3	US-08-307-896-1

28	42	65.6	394	4	US-09-442-349A-106	Sequence 106, App
29	42	65.6	394	4	US-09-963-137-192	Sequence 132, App
30	42	65.6	394	4	US-09-963-137-194	Sequence 194, App
31	42	65.6	394	5	PCT-US95-11808-1	Sequence 1, Appli
32	42	65.6	409	4	US-09-902-340-12745	Sequence 12745, A
33	42	65.6	775	4	US-09-513-838-6	Sequence 6, Appli
34	42	65.6	1181	4	US-09-826-509-587	Sequence 587, Appl
35	41.5	64.8	28	3	US-08-817-811-67	Sequence 67, Appl
36	41	64.1	12	3	US-08-817-811-29	Sequence 29, Appl
37	41	64.1	514	2	US-08-960-022-14	Sequence 14, Appl
38	40	62.5	28	3	US-08-817-811-15	Sequence 15, Appl
39	39	60.9	64	4	US-09-583-110-4222	Sequence 4222, Ap
40	39	60.9	85	4	US-09-513-999C-4696	Sequence 4696, Ap
41	39	60.9	96	4	US-09-107-433-3416	Sequence 3416, Ap
42	39	60.9	459	4	US-09-270-767-45471	Sequence 45471, A
43	38	59.4	8	3	US-08-817-811-8	Sequence 8, Appli
44	38	59.4	19	6	5304631-14	Patent No. 5304631
45	38	59.4	19	6	5304631-14	Patent No. 5304631

ALIGNMENTS

RESULT 1
US-08-817-811-1
; Sequence 1, Application US/08817811
; Patent No. 6174528
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
; APPLICANT: Relif, Wendy A.
; APPLICANT: Good, Michael F.
; APPLICANT: Saul, Allan J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
; TITLE OF INVENTION: COMPRISING SAME
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,811
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 96/11944
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC:005
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-817-811-1

Query Match 100.0%; Score 64; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
 Db 7 ASREAKKQVEKALE 20

RESULT 2

US-08-937-271-11
 ; Sequence 11, Application US/08937271
 ; Patent No. 6063386
 ; GENERAL INFORMATION:
 ; APPLICANT: Dale, James B.
 ; APPLICANT: Lederer, James W.
 ; TITLE OF INVENTION: RECOMBINANT MULTIVALENT M PROTEIN
 ; TITLE OF INVENTION: VACCINE
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED and BERRY
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/937,271
 ; FILING DATE: 15-SEP-1997
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rosenman, Stephen J.
 ; REGISTRATION NUMBER: 43,058
 ; REFERENCE/DOCKET NUMBER: 481112.405C1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 236 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-937-271-11

Query Match 100.0%; Score 64; DB 3; Length 236;
 Best Local Similarity 100.0%; Pred. No. 0.0084;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
 Db 87 ASREAKKQVEKALE 100

RESULT 3

US-08-914-479A-4
 ; Sequence 4, Application US/08914479A
 ; Patent No. 6419932
 ; GENERAL INFORMATION:
 ; APPLICANT: Dale, James B.
 ; TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
 ; TITLE OF INVENTION: FOR GROUP A STREPTOCOCCAL VACCINE
 ; FILE REFERENCE: 481112.404C2
 ; CURRENT APPLICATION NUMBER: US/08/914,479A
 ; CURRENT FILING DATE: 1997-08-19
 ; PRIOR APPLICATION NUMBER: 08/409,270
 ; PRIOR FILING DATE: 1995-03-23
 ; PRIOR APPLICATION NUMBER: 07/945,860
 ; PRIOR FILING DATE: 1992-09-16
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4

; LENGTH: 254
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: An antigen of M5 and a carrier of the
 ; OTHER INFORMATION: COOH-terminal portion of M5
 ; US-08-914-479A-4

Query Match 100.0%; Score 64; DB 4; Length 254;
 Best Local Similarity 100.0%; Pred. No. 0.009;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
 Db 105 ASREAKKQVEKALE 118

RESULT 4

US-08-914-479A-6
 ; Sequence 6, Application US/08914479A
 ; Patent No. 6419932
 ; GENERAL INFORMATION:
 ; APPLICANT: Dale, James B.
 ; TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
 ; TITLE OF INVENTION: FOR GROUP A STREPTOCOCCAL VACCINE
 ; FILE REFERENCE: 481112.404C2
 ; CURRENT APPLICATION NUMBER: US/08/914,479A
 ; CURRENT FILING DATE: 1997-08-19
 ; PRIOR APPLICATION NUMBER: 08/409,270
 ; PRIOR FILING DATE: 1995-03-23
 ; PRIOR APPLICATION NUMBER: 07/945,860
 ; PRIOR FILING DATE: 1992-09-16
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 284
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: An antigen of three fragments of M5 and a carrier
 ; OTHER INFORMATION: of the COOH-terminal portion of M5
 ; US-08-914-479A-6

Query Match 100.0%; Score 64; DB 4; Length 284;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
 Db 135 ASREAKKQVEKALE 148

RESULT 5

US-08-937-271-10
 ; Sequence 10, Application US/08937271
 ; Patent No. 6063386
 ; GENERAL INFORMATION:
 ; APPLICANT: Dale, James B.
 ; APPLICANT: Lederer, James W.
 ; TITLE OF INVENTION: RECOMBINANT MULTIVALENT M PROTEIN
 ; TITLE OF INVENTION: VACCINE
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED and BERRY
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/937,271
;; FILING DATE: 15-SEP-1997
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rosenman, Stephen J.
;; REGISTRATION NUMBER: 43,058
;; REFERENCE/DOCKET NUMBER: 481112.405C1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 305 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-937-271-10

Query Match 100.0%; Score 64; DB 3; Length 305;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
Db 156 ASREAKKQVEKALE 169
|||||

RESULT 6
US-08-302-756E-35

;; Sequence 35, Application US/08302756E
;; Patent No. 6737521
;; GENERAL INFORMATION:
;; APPLICANT: FISCHETTI, Vincent A.
;; APPLICANT: POZZI, Gianni
;; APPLICANT: SCHNEEWIND, Olaf
;; TITLE OF INVENTION: DELIVERY AND EXPRESSION OF A HYBRID SURFACE PROTEIN ON
;; TITLE OF INVENTION: THE SURFACE OF GRAM POSITIVE BACTERIA
;; FILE REFERENCE: 016921-076
;; CURRENT APPLICATION NUMBER: US/08/302,756E
;; CURRENT FILING DATE: 1995-03-07
;; PRIOR APPLICATION NUMBER: US 07/522,440
;; PRIOR FILING DATE: 1990-05-11
;; PRIOR APPLICATION NUMBER: US 07/742,199
;; PRIOR FILING DATE: 1991-08-05
;; PRIOR APPLICATION NUMBER: US 07/814,823
;; PRIOR FILING DATE: 1991-12-23
;; PRIOR APPLICATION NUMBER: US 07/851,082
;; PRIOR FILING DATE: 1992-03-13
;; PRIOR APPLICATION NUMBER: PCT/US93/02355
;; PRIOR FILING DATE: 1993-03-12
;; NUMBER OF SEQ ID NOS: 61
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 35
;; LENGTH: 440
;; TYPE: PRT
;; ORGANISM: S. pyogenes
US-08-302-756E-35

Query Match 100.0%; Score 64; DB 4; Length 440;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
Db 292 ASREAKKQVEKALE 305
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RESULT 7

US-08-795-475-6
;; Sequence 6, Application US/08795475
;; Patent No. 5965390

;; GENERAL INFORMATION:
;; APPLICANT: Björck, Lars
;; APPLICANT: Sjöbring, Ulf
;; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
;; NUMBER OF SEQUENCES: 14
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SEED and BERRY LLP
;; STREET: 6300 Columbia Center, 701 Fifth Avenue
;; CITY: Seattle
;; STATE: Washington
;; COUNTRY: USA
;; ZIP: 98104-7092
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/795,475
;; FILING DATE: 11-FEB-1997
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McWaters, David D.
;; REGISTRATION NUMBER: 33,963
;; REFERENCE/DOCKET NUMBER: 100084.402D1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 443 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-795-475-6

Query Match 100.0%; Score 64; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
Db 294 ASREAKKQVEKALE 307
|||||

RESULT 8

US-08-325-278B-6
;; Sequence 6, Application US/08325278B
;; Patent No. 6822075
;; GENERAL INFORMATION:
;; APPLICANT: Björck, Lars
;; APPLICANT: Sjöbring, Ulf
;; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Seed IP Law Group
;; STREET: 701 Fifth Avenue Suite 6300
;; CITY: Seattle
;; STATE: Washington
;; COUNTRY: USA
;; ZIP: 98104-7092
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/325,278B
;; FILING DATE: 26-Oct-1994
;; CLASSIFICATION: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Potter, Jane E. R.
;; REGISTRATION NUMBER: 33,332

REFERENCE/DOCKET NUMBER: 100084.402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 443 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-325-2788-6

Query Match 100.0%; Score 64; DB 4; Length 443;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
Db 294 ASREAKKQVEKALE 307

RESULT 9
US-08-817-811-34
; Sequence 34, Application US/08817811
; Patent No. 6174528
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
; APPLICANT: Relf, Wendy A.
; APPLICANT: Good, Michael F.
; APPLICANT: Saul, Allan J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,811
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 96/11944
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC:005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-817-811-34

Query Match 87.5%; Score 56; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 REAKKQVEKALE 14

Db 1 REAKKQVEKALE 12

RESULT 10
US-08-817-811-11
; Sequence 11, Application US/08817811
; Patent No. 6174528
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
; APPLICANT: Relf, Wendy A.
; APPLICANT: Good, Michael F.
; APPLICANT: Saul, Allan J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,811
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 96/11944
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC:005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-817-811-11

Query Match 85.9%; Score 55; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKA 12
Db 1 ASREAKKQVEKA 12

RESULT 11
US-08-817-811-32
; Sequence 32, Application US/08817811
; Patent No. 6174528
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
; APPLICANT: Relf, Wendy A.
; APPLICANT: Good, Michael F.
; APPLICANT: Saul, Allan J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee

```

; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,811
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 96/11944
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC:005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-08-817-811-32

Query Match 85.9%; Score 55; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKA 12
Db 1 ASREAKKQVEKA 12

RESULT 12
US-08-817-811-33
; Sequence 33, Application US/08817811
; Patent No. 6174528
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
; APPLICANT: Relf, Wendy A.
; APPLICANT: Good, Michael F.
; APPLICANT: Saul, Allan J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,811
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 96/11944
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC:005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-08-817-811-33

Query Match 81.2%; Score 52; DB 3; Length 28;
Best Local Similarity 78.6%; Pred. No. 0.075;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC:005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-08-817-811-33

Query Match 85.9%; Score 55; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SREAKKQVEKAL 13
Db 1 SREAKKQVEKAL 12

RESULT 13
US-08-817-811-18
; Sequence 18, Application US/08817811
; Patent No. 6174528
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
; APPLICANT: Relf, Wendy A.
; APPLICANT: Good, Michael F.
; APPLICANT: Saul, Allan J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,811
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 96/11944
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC:005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-08-817-811-18

Query Match 81.2%; Score 52; DB 3; Length 28;
Best Local Similarity 78.6%; Pred. No. 0.075;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ASREAKKQVEKALE 14
Db 10 ASREAKKQVEKVK 23

RESULT 14

US-08-817-811-31
; Sequence 31, Application US/08817811
; Patent No. 6174528
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
; APPLICANT: Relf, Wendy A.
; APPLICANT: Good, Michael F.
; APPLICANT: Saul, Allan J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,811
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 96/11944
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC:005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-817-811-31

Query Match 79.7%; Score 51; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEK 11
Db 2 ASREAKKQVEK 12

RESULT 15

US-08-817-811-17
; Sequence 17, Application US/08817811
; Patent No. 6174528
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
; APPLICANT: Relf, Wendy A.
; APPLICANT: Good, Michael F.
; APPLICANT: Saul, Allan J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,811
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 96/11944
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC:005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-817-811-17

Query Match 74.2%; Score 47.5; DB 3; Length 28;
Best Local Similarity 76.5%; Pred. No. 0.38;
Matches 13; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 1 ASREAKKQVE---KALE 14
Db 11 ASREAKKQVEDKVKQLE 27

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Job time : 20.5349 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2005, 08:36:38 ; Search time 68.3721 Seconds
(without alignments)
79.939 Million cell updates/sec

Title: US-10-706-275-1

Perfect score: 64

Sequence: 1 ASREAKKQVEKALE 14

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*

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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	64	100.0	20	13	US-10-044-034-22
3	64	100.0	20	17	US-10-706-275-5
4	64	100.0	29	17	US-10-706-275-2
5	64	100.0	29	17	US-10-706-275-15
6	64	100.0	254	13	US-10-141-627-4
7	64	100.0	284	13	US-10-141-627-6
8	64	100.0	443	8	US-08-325-278-6
9	64	100.0	553	16	US-10-474-792-672
10	64	100.0	558	17	US-10-732-923-3295
11	57	89.1	28	17	US-10-706-275-12

12	56	87.5	28	17	US-10-706-275-13	Sequence 13, Appl
13	56	87.5	28	17	US-10-706-275-14	Sequence 14, Appl
14	52	81.2	28	17	US-10-706-275-11	Sequence 11, Appl
15	47.5	74.2	28	17	US-10-706-275-10	Sequence 10, Appl
16	45	70.3	546	15	US-10-369-493-5342	Sequence 5342, Ap
17	44.5	69.5	28	17	US-10-706-275-9	Sequence 9, Appl1
18	42	65.6	65	10	US-09-309-196-83	Sequence 83, Appl
19	42	65.6	65	15	US-10-263-341-83	Sequence 83, Appl
20	42	65.6	65	16	US-10-600-003-83	Sequence 83, Appl
21	42	65.6	86	15	US-10-424-599-223904	Sequence 223904,
22	42	65.6	377	17	US-10-732-923-7618	Sequence 7618, Ap
23	42	65.6	379	10	US-09-952-680A-15	Sequence 15, Appl
24	42	65.6	379	16	US-10-408-765A-105	Sequence 105, App
25	42	65.6	379	16	US-10-215-982-15	Sequence 15, Appl
26	42	65.6	379	17	US-10-732-923-7963	Sequence 7963, Ap
27	42	65.6	379	17	US-10-732-923-8015	Sequence 8015, Ap
28	42	65.6	380	10	US-09-952-680A-16	Sequence 16, Appl
29	42	65.6	380	16	US-10-215-982-16	Sequence 16, Appl
30	42	65.6	380	17	US-10-732-923-8016	Sequence 8016, Ap
31	42	65.6	380	17	US-10-732-923-8055	Sequence 8055, Ap
32	42	65.6	384	17	US-10-732-923-8022	Sequence 8022, Ap
33	42	65.6	388	17	US-10-732-923-8054	Sequence 8054, Ap
34	42	65.6	384	10	US-09-952-680A-13	Sequence 13, Appl
35	42	65.6	394	10	US-09-963-131-192	Sequence 192, App
36	42	65.6	394	10	US-09-963-131-194	Sequence 194, App
37	42	65.6	394	15	US-10-116-275-187	Sequence 187, Appl
38	42	65.6	394	15	US-10-352-843-18	Sequence 18, Appl
39	42	65.6	394	16	US-10-215-982-13	Sequence 13, Appl
40	42	65.6	394	16	US-10-684-422-194	Sequence 194, App
41	42	65.6	394	17	US-10-732-923-7589	Sequence 7589, Ap
42	42	65.6	394	17	US-10-732-923-7592	Sequence 7592, Ap
43	42	65.6	394	17	US-10-732-923-7620	Sequence 7620, Ap
44	42	65.6	394	17	US-10-732-923-7653	Sequence 7653, Ap
45	42	65.6	394	17	US-10-732-923-8017	Sequence 8017, Ap

ALIGNMENTS

RESULT 1

US-10-706-275-1

; Sequence 1, Application US/10706275

; Publication No. US20050002956A1

; GENERAL INFORMATION:

; APPLICANT: ID Biomedical Corporation of Quebec

; APPLICANT: The Council of the Queensland Institute of Medical Research

; APPLICANT: Lowell, George H.

; APPLICANT: Burt, David S.

; APPLICANT: White, Gregory L.

; APPLICANT: Good, Michael F.

; APPLICANT: Batzloff, Michael R.

; APPLICANT: Leanderson, Tomas B.

; TITLE OF INVENTION: Vaccine

; FILE REFERENCE: 021989-000710US

; CURRENT APPLICATION NUMBER: US/10/706,275

; CURRENT FILING DATE: 2003-11-13

; PRIOR APPLICATION NUMBER: US 60/426,409

; PRIOR FILING DATE: 2002-11-15

; PRIOR APPLICATION NUMBER: AU 2002302132

; PRIOR FILING DATE: 2002-11-15

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: antigenic peptide sequence derivative of S. pyogenes

Query Match 100.0%; Score 64; DB 17; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
|||||
Db 1 ASREAKKQVEKALE 14

RESULT 2

US-10-044-034-22
; Sequence 22, Application US/10044034
; Publication No. US20020169264A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, DAVID C.
; APPLICANT: O'BRIEN-SIMPSON, NEIL M.
; APPLICANT: BROWN, LORENA E.
; APPLICANT: EDE, NICHOLAS J.
; APPLICANT: BRANDT, EVELYN R.
; APPLICANT: GOOD, MICHAEL F.
; TITLE OF INVENTION: POLYMERS INCORPORATING PEPTIDES
; FILE REFERENCE: FERC-006
; CURRENT APPLICATION NUMBER: US/10/044,034
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: P05071
; PRIOR FILING DATE: 1997-02-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptides
US-10-044-034-22

Query Match 100.0%; Score 64; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
|||||
Db 7 ASREAKKQVEKALE 20

RESULT 3

US-10-706-275-5
; Sequence 5, Application US/10706275
; Publication No. US2005002956A1
; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec
; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.
; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.
; APPLICANT: Good, Michael F.
; APPLICANT: Batzloff, Michael R.
; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10/706,275
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence p145
US-10-706-275-5

Query Match 100.0%; Score 64; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASREAKKQVEKALE 14
|||||
Db 7 ASREAKKQVEKALE 20

RESULT 4

US-10-706-275-2
; Sequence 2, Application US/10706275
; Publication No. US20050002956A1
; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec
; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.
; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.
; APPLICANT: Good, Michael F.
; APPLICANT: Batzloff, Michael R.
; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10/706,275
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide derivative of S. pyogenes with flanking sequen
; OTHER INFORMATION: es
US-10-706-275-2

Query Match 100.0%; Score 64; DB 17; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
|||||
Db 9 ASREAKKQVEKALE 22

RESULT 5

US-10-706-275-15
; Sequence 15, Application US/10706275
; Publication No. US20050002956A1
; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec
; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.
; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.
; APPLICANT: Good, Michael F.
; APPLICANT: Batzloff, Michael R.
; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10/706,275
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence p145
US-10-706-275-5

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-15

Query Match 100.0%; Score 64; DB 17; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
| | | | | | | | | | | | | | | |
Db 9 ASREAKKQVEKALE 22

RESULT 6
US-10-141-627-4
; Sequence 4, Application US/10141627
; Publication No. US20020176863A1
; GENERAL INFORMATION:
; APPLICANT: Dale, James B.
; TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
; FILE OF INVENTION: FOR GROUP A STREPTOCOCCAL VACCINE
; FILE REFERENCE: 481112.404C3
; CURRENT APPLICATION NUMBER: US/10/141.627
; CURRENT FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: An antigen of M5 and a carrier of the
; OTHER INFORMATION: COOH-terminal portion of M5
US-10-141-627-4

Query Match 100.0%; Score 64; DB 13; Length 254;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
| | | | | | | | | | | | | | | |
Db 105 ASREAKKQVEKALE 118

RESULT 7
US-10-141-627-6
; Sequence 6, Application US/10141627
; Publication No. US20020176863A1
; GENERAL INFORMATION:
; APPLICANT: Dale, James B.
; TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
; FILE OF INVENTION: FOR GROUP A STREPTOCOCCAL VACCINE
; FILE REFERENCE: 481112.404C3
; CURRENT APPLICATION NUMBER: US/10/141.627
; CURRENT FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: An antigen of three fragments of M5 and a carrier
; OTHER INFORMATION: of the COOH-terminal portion of M5
US-10-141-627-6

Query Match 100.0%; Score 64; DB 13; Length 284;
Best Local Similarity 100.0%; Pred. No. 0.055;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASREAKKQVEKALE 14
| | | | | | | | | | | | | | | |
Db 135 ASREAKKQVEKALE 148

RESULT 8
US-08-325-278-6
; Sequence 6, Application US/08325278
; Publication No. US20030027283A1
; GENERAL INFORMATION:
; APPLICANT: Bjvick, Lars
; APPLICANT: Sjvbring, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/325,278
; APPLICATION NUMBER: US/08/325,278
; FILING DATE: 26-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 450023.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-325-278-6

Query Match 100.0%; Score 64; DB 8; Length 443;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
| | | | | | | | | | | | | | | |
Db 294 ASREAKKQVEKALE 307

RESULT 9
US-10-474-792-672
; Sequence 672, Application US/10474792
; Publication No. US20040236072A1
; GENERAL INFORMATION:
; APPLICANT: Olmsted, Stephen
; APPLICANT: Zagureky, Robert
; APPLICANT: Nickbarg, Elliot
; APPLICANT: Winter, Lourie
; TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
; FILE REFERENCE: AM 100399
; CURRENT APPLICATION NUMBER: US/10/474,792
; CURRENT FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 672
; LENGTH: 553

; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-474-792-672

Query Match 100.0%; Score 64; DB 16; Length 553;
Best Local Similarity 100.0%; Pred. No. 0.11; Length 553;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
| | | | | | | | | | | | | | | |
DB 404 ASREAKKQVEKALE 417

RESULT 10

US-10-732-923-3295
; Sequence 3295, Application US/10732923
; Publication No. US20050108791A1

; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D

; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C

; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10

; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04

; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 3295

; LENGTH: 558
; TYPE: PRT

; ORGANISM: Streptococcus pyogenes
US-10-732-923-3295

Query Match 100.0%; Score 64; DB 17; Length 558;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
| | | | | | | | | | | | | | | |
DB 409 ASREAKKQVEKALE 422

RESULT 11

US-10-706-275-12
; Sequence 12, Application US/10706275
; Publication No. US20050002956A1

; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec

; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.

; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.

; APPLICANT: Good, Michael F.
; APPLICANT: Batzloff, Michael R.

; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine

; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10/706,275

; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409

; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132

; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: Patent in version 3.1
; SEQ ID NO 12

; LENGTH: 28
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-12

Query Match 89.1%; Score 57; DB 17; Length 28;

Best Local Similarity 85.7%; Pred. No. 0.061;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
| | | | | | | | | | | | | | | |
DB 9 ASREAKKQVEKAVK 22

RESULT 12

US-10-706-275-13

; Sequence 13, Application US/10706275
; Publication No. US20050002956A1

; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec

; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.

; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.

; APPLICANT: Good, Michael F.
; APPLICANT: Batzloff, Michael R.

; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine

; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10/706,275

; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409

; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132

; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: Patent in version 3.1
; SEQ ID NO 13

; LENGTH: 28
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-13

Query Match 87.5%; Score 56; DB 17; Length 28;

Best Local Similarity 92.3%; Pred. No. 0.087;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SREAKKQVEKALE 14
| | | | | | | | | | | | | | | |
DB 9 SREAKKQVEKALK 21

RESULT 13

US-10-706-275-14

; Sequence 14, Application US/10706275
; Publication No. US20050002956A1

; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec

; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.

; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.

; APPLICANT: Good, Michael F.
; APPLICANT: Batzloff, Michael R.

; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine

; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10/706,275

; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409

; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132

; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14

; LENGTH: 28

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-14
Query Match      87.5%; Score 56; DB 17; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 REAKKQVEKALE 14
    |||||
Db 9 REAKKQVEKALE 20

RESULT 14
US-10-706-275-11
; Sequence 11, Application US/10706275
; Publication No. US20050002956A1
; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec
; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.
; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.
; APPLICANT: Good, Michael F.
; APPLICANT: Batzloff, Michael R.
; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10706,275
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-11
Query Match      81.2%; Score 52; DB 17; Length 28;
Best Local Similarity 78.6%; Pred. No. 0.36;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
    |||||
Db 10 ASREAKKQVEKVK 23

RESULT 15
US-10-706-275-10
; Sequence 10, Application US/10706275
; Publication No. US20050002956A1
; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec
; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.
; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.
; APPLICANT: Good, Michael F.
; APPLICANT: Batzloff, Michael R.
; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10706,275
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409
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; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-10
Query Match      74.2%; Score 47.5; DB 17; Length 28;
Best Local Similarity 76.5%; Pred. No. 1.8;
Matches 13; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

Qy 1 ASREAKKQVE---KALE 14
    |||||
Db 11 ASREAKKQVEDKVKQLE 27

Search completed: August 4, 2005, 08:55:13
Job time : 68.3721 secs
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Db 266 ASREAKKQVEKALE 279

RESULT 2

S30283

protein M precursor - Streptococcus pyogenes (serotype M41)

C;Species: Streptococcus pyogenes

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: S30283; S29680

R;Podbielski, A.

Mol. Gen. Genet. 237, 287-300, 1993

A;Title: Three different types of organization of the vir regulon in group A streptococci

A;Reference number: S30283; MUID:93204905; PMID:8455563

A;Accession: S30283

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-408 <POD1>

A;Cross-references: UNIPROT:Q54837; EMBL:X58178

R;Podbielski, A.; Melzer, B.

submitted to the EMBL Data Library, February 1991

A;Description: Per mediated cloning and sequencing of group A streptococcal emm41/52 (ev

A;Reference number: S29680

A;Accession: S29680

A;Molecule type: DNA

A;Residues: 1-230,'N',232-371,'R',373-408 <POD2>

A;Cross-references: EMBL:X58178; NID:g47362; PIDN:CAA41167.1; PID:g47363

C;Genetics:

A;Gene: emm

C;Superfamily: M5 protein

C;Keywords: transmembrane protein

F;1-41/Domain: signal sequence #status predicted <SIG>

F;42-408/Product: M protein #status predicted <MAT>

F;383-401/Domain: transmembrane #status predicted <TM>

Query Match

Best Local Similarity 100.0%; Score 64; DB 2; Length 408;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14

|||||

Db 259 ASREAKKQVEKALE 272

RESULT 3

S30284

M protein precursor - Streptococcus pyogenes (serotype M52)

C;Species: Streptococcus pyogenes

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: S30284; S29681

R;Podbielski, A.

Mol. Gen. Genet. 237, 287-300, 1993

A;Title: Three different types of organization of the vir regulon in group A streptococci

A;Reference number: S30283; MUID:93204905; PMID:8455563

A;Accession: S30284

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-436 <POD1>

A;Cross-references: UNIPROT:Q54839; EMBL:X58179

R;Podbielski, A.; Melzer, B.

submitted to the EMBL Data Library, February 1991

A;Description: Per mediated cloning and sequencing of group A streptococcal emm41/52 (ev

A;Reference number: S29680

A;Accession: S29681

A;Molecule type: DNA

A;Residues: 1-216,'N',218-436 <POD2>

A;Cross-references: EMBL:X58179; NID:g47364; PIDN:CAA41168.1; PID:g47365

C;Genetics:

A;Gene: emm

C;Superfamily: M5 protein

C;Keywords: transmembrane protein

F;1-41/Domain: signal sequence #status predicted <SIG>

F;42-436/Product: M protein #status predicted <MAT>

F;411-429/Domain: transmembrane #status predicted <TM>

Query Match 100.0%; Score 64; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14

|||||

Db 287 ASREAKKQVEKALE 300

RESULT 4

S43556

plasminogen-binding protein MLC36 - Streptococcus sp. (fragment)

C;Species: Streptococcus sp.

C;Date: 14-Sep-1994 #sequence_revision 03-Nov-1995 #text_change 26-Aug-1999

C;Accession: S45598; S43556

R;ben Nasr, A.; Wistedt, A.; Ringdahl, U.; Sjoebing, U.

Eur. J. Biochem. 222, 267-276, 1994

A;Title: Streptokinase activates plasminogen bound to human group C and G streptococci

A;Reference number: S45598; MUID:94291620; PMID:8020466

A;Accession: S45598

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-454 <BE2>

A;Cross-references: EMBL:Z32677; NID:g474767; PIDN:CAA83588.1; PID:g474768

C;Superfamily: M5 protein

Query Match

Best Local Similarity 100.0%; Score 64; DB 2; Length 454;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14

|||||

Db 332 ASREAKKQVEKALE 345

RESULT 5

S43554

plasminogen-binding protein MLG72 - Streptococcus sp. (fragment)

C;Species: Streptococcus sp.

A;Variety: group G

C;Date: 07-Sep-1994 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000

C;Accession: S45599; S43554

R;ben Nasr, A.; Wistedt, A.; Ringdahl, U.; Sjoebing, U.

Eur. J. Biochem. 222, 267-276, 1994

A;Title: Streptokinase activates plasminogen bound to human group C and G streptococci

A;Reference number: S45598; MUID:94291620; PMID:8020466

A;Accession: S45599

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-472 <BE2>

A;Cross-references: EMBL:Z32678; NID:g474769; PIDN:CAA83589.1; PID:g1333838

C;Superfamily: M5 protein

Query Match

Best Local Similarity 100.0%; Score 64; DB 2; Length 472;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14

|||||

Db 350 ASREAKKQVEKALE 363

RESULT 6

A26297

M6 protein - Streptococcus pyogenes

C;Species: Streptococcus pyogenes

C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004

C;Accession: A26297

R;Hollingshead, S.K.; Fischetti, V.A.; Scott, J.R.

J. Biol. Chem. 261, 1677-1686, 1986

A;Title: Complete nucleotide sequence of type 6 M protein of the group A streptococcus.

A;Reference number: A26297; MUID:86111835; PMID:3511046

A;Accession: A26297
A;Molecule type: DNA
A;Residues: 1-483 <HOL>
A;Cross-references: UNIPROT:P08089; GB:M11338; GB:M11415; NID:G153699; PIDN:AAA26920.1;
C;Genetics:
A;Gene: emm6
C;Superfamily: M5 protein
C;Keywords: coiled coil; transmembrane protein

Query Match 100.0%; Score 64; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
| | | | | | | | | | | | | | | |
Db 334 ASREAKKQVEKALE 347

RESULT 7
S35401
M1 protein precursor - Streptococcus pyogenes
C;Species: Streptococcus pyogenes
A;Variety: serotype M1
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S35401; S61074; S60784
R;Pdbielecki, A.
submitted to the EMBL Data Library, September 1991
A;Reference number: S35401
A;Accession: S35401
A;Molecule type: DNA
A;Residues: 1-484 <PDB>
A;Cross-references: UNIPROT:Q10372; EMBL:X62131; NID:G311757; PIDN:CAA44062.1; PID:G311757
R;Whatmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
submitted to the EMBL Data Library, July 1994
A;Description: Noncongruent relationships between variation in emm1 gene sequences and t
A;Reference number: S61072
A;Accession: S61074
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 16-94 <WHA>
A;Cross-references: EMBL:U11940; NID:G533557; PIDN:AAA99556.1; PID:G533558
R;Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
A;Title: Non-congruent relationships between variation in emm gene sequences and the p
A;Reference number: S60784; MUID:95198537; PMID:7891551
A;Accession: S60784
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 29-89 <WH2>
A;Cross-references: EMBL:U11940
C;Genetics:
A;Gene: emm1
C;Superfamily: M5 protein

Query Match 100.0%; Score 64; DB 2; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
| | | | | | | | | | | | | | | |
Db 335 ASREAKKQVEKALE 348

RESULT 8
S46489
M1 protein precursor - Streptococcus pyogenes
C;Species: Streptococcus pyogenes
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S46489; S46490
R;Akesson, P.; Schmidt, K.H.; Cooney, J.; Bioerck, L.
Biochem. J. 300, 877-886, 1994
A;Title: M1 protein and protein H: IgGFc- and albumin-binding streptococcal surface prot
A;Reference number: S46489; MUID:94280417; PMID:8010973

A;Accession: S46489
A;Molecule type: DNA
A;Residues: 1-484 <AKE>
A;Cross-references: UNIPROT:Q05464; UNIPROT:Q10372; UNIPROT:Q99XV0
A;Experimental source: strain 40/58, serotype M1
A;Accession: S46490
A;Molecule type: protein
A;Residues: 42-51 <AKW>
A;Experimental source: strain 40/58, serotype M1
C;Genetics:
A;Gene: emm1
C;Superfamily: M5 protein
C;Keywords: transmembrane protein
F;1-41/Domain: signal sequence #status predicted <SIG>
F;42-484/Product: M1 protein #status experimental <MAT>
F;459-477/Domain: transmembrane #status predicted <TMM>

Query Match 100.0%; Score 64; DB 2; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
| | | | | | | | | | | | | | | |
Db 335 ASREAKKQVEKALE 348

RESULT 9
S34978
M1.1 protein precursor - Streptococcus pyogenes
C;Species: Streptococcus pyogenes
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S34978; S31966
R;Harbaugh, M.P.; Podbielski, A.; Huegl, S.; Cleary, P.P.
Mol. Microbiol. 8, 981-991, 1993
A;Title: Nucleotide substitutions and small-scale insertion produce size and antigenic
A;Reference number: S34978; MUID:93360826; PMID:8355619
A;Accession: S34978
A;Molecule type: DNA
A;Residues: 1-484 <HAR>
A;Cross-references: UNIPROT:Q05464; EMBL:Z21845; NID:G49401; PIDN:CAA79893.1; PID:G49401
C;Genetics:
A;Gene: emm1.1
C;Superfamily: M5 protein
C;Keywords: membrane protein
F;1-42/Domain: signal sequence #status predicted <SIG>
F;43-484/Product: M1.1 protein #status predicted <MAT>

Query Match 100.0%; Score 64; DB 2; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
| | | | | | | | | | | | | | | |
Db 335 ASREAKKQVEKALE 348

RESULT 10
A28616
M5 protein precursor - Streptococcus pyogenes
C;Species: Streptococcus pyogenes
A;Variety: serotype M5
C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 09-Jul-2004
C;Accession: A28616; S60787
R;Miller, L.; Gray, L.; Beachey, E.; Kehoe, M.
J. Biol. Chem. 263, 5668-5673, 1988
A;Title: Antigenic variation among group A streptococcal M proteins. Nucleotide sequenc
A;Reference number: A28616; MUID:88186881; PMID:3281944
A;Accession: A28616
A;Molecule type: DNA
A;Residues: 1-492 <MIL>
A;Cross-references: UNIPROT:P02977; GB:M20374; NID:G153812; PIDN:AAA26976.1; PID:G15381
R;Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994

A;Title: Non-congruent relationships between variation in emm gene sequences and the po
A;Reference number: S60784; MUID:95198537; PMID:7891551
A;Accession: S60787
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 30-89 <WHA>
C;Genetics:
A;Gene: smps
C;Superfamily: M5 protein
C;Keywords: coiled coil; transmembrane protein
F;1-42/Domain: signal sequence #status Predicted <SIG>
F;43-492/Product: M5 protein #status Predicted <MAT>

Query Match 100.0%; Score 64; DB 2; Length 492;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
|||||

Db 343 ASREAKKQVEKALE 356
|||||

RESULT 11
A44643
M protein precursor - Streptococcus pyogenes (serotype M57) (fragment)
C;Species: Streptococcus pyogenes
A;Variety: serotype M57
C;Date: 26-Sep-1994 #sequence_revision 10-Nov-1994 #text_change 10-Dec-1999
C;Accession: A44643; S60833
R;Manjula, B.N.; Khandke, K.M.; Fairwell, T.; Relf, W.A.; Sriprakash, K.S.
J. Protein Chem. 10, 369-384, 1991
A;Title: Heptad motifs within the distal subdomain of the coiled-coil rod region of M pr
her: nucleotide sequence of the M57 gene and relation of the dedu.
A;Reference number: A44643; MUID:92143933; PMID:1781883
A;Accession: A44643
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-501 <MAN>
A;Experimental source: type M57, strain A995
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:83737, NCBI:P:83738)
A;Note: parts of this sequence were confirmed by peptide sequencing
R;Whitmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
A;Title: Non-congruent relationships between variation in emm gene sequences and the po
A;Reference number: S60784; MUID:95198537; PMID:7891551
A;Accession: S60833
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 14-95 <WHA>
A;Cross-references: EMBL:U11971
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C;Superfamily: M5 protein
C;Keywords: coiled coil; dimer

Query Match 100.0%; Score 64; DB 2; Length 501;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
|||||

Db 364 ASREAKKQVEKALE 377
|||||

RESULT 12
S57835
IGG-binding protein emm1 precursor - Streptococcus pyogenes (strain 64/14)
N;Alternate names: IGG-binding protein type IIA; type IIA immunoglobulin G-binding prote
C;Species: Streptococcus pyogenes
A;Variety: strain 64/14
C;Date: 28-Nov-1995 #sequence_revision 09-Mar-1996 #text_change 09-Jul-2004
C;Accession: S57835; S58931
R;Boyle, M.D.P.; Hawlitzky, J.; Raeder, R.; Podbielski, A.

Infect. Immun. 62, 1336-1347, 1994
A;Title: Analysis of genes encoding two unique type IIA immunoglobulin G-binding protein
A;Reference number: S57834; MUID:94178942; PMID:8132341
A;Accession: S57835
A;Molecule type: DNA
A;Residues: 1-528 <BOY>
A;Cross-references: UNIPROT:Q54843; EMBL:X72932
A;Experimental source: strain 64/14
A;Note: the authors translated the codons CTTAAA for residue 52 and 53 as Arg
R;Podbielski, A.
submitted to the EMBL Data Library, March 1993
A;Reference number: S58931
A;Accession: S58931
A;Molecule type: DNA
A;Residues: 1-46,'E',48-52,'E',54-528 <POD>
A;Cross-references: EMBL:X72932; NID:g507128; PIDN:CAA51437.1; PID:g507130
A;Experimental source: strain 64/14
C;Genetics:
A;Gene: emmL
C;Superfamily: M5 protein
F;1-41/Domain: signal sequence #status Predicted <SIG>
F;42-528/Product: type IIA immunoglobulin G-binding protein emm1 #status Predicted <MAT>

Query Match 100.0%; Score 64; DB 2; Length 528;
Best Local Similarity 100.0%; Pred. No. 0.026; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
|||||

Db 379 ASREAKKQVEKALE 392
|||||

RESULT 13
S54871
M protein - Streptococcus sp.
C;Species: Streptococcus sp.
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S54871
R;Podbielski, A.; Melzer, B.
submitted to the EMBL Data Library, June 1991
A;Reference number: S54871
A;Accession: S54871
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-532 <POD>
A;Cross-references: UNIPROT:Q55098; EMBL:X60037; NID:g840905; PIDN:CAA42693.1; PID:g840905
C;Superfamily: M5 protein

Query Match 100.0%; Score 64; DB 2; Length 532;
Best Local Similarity 100.0%; Pred. No. 0.026; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
|||||

Db 383 ASREAKKQVEKALE 396
|||||

RESULT 14
A28549
M24 protein precursor - Streptococcus pyogenes
C;Species: Streptococcus pyogenes
A;Variety: serotype M24
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A28549; S60802
R;Mouw, A.R.; Beachey, E.H.; Burdett, V.
J. Bacteriol. 170, 676-684, 1988
A;Title: Molecular evolution of streptococcal M protein: cloning and nucleotide sequence
A;Reference number: A28549; MUID:88115166; PMID:3276665
A;Accession: A28549
A;Molecule type: DNA
A;Residues: 1-539 <NOU>
A;Cross-references: UNIPROT:P12379; GB:M19031; NID:g153616; PIDN:AAA26874.1; PID:g153617
R;Whitmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.

Mol. Microbiol. 14, 619-631, 1994
A;Title: Non-congruent relationships between variation in emm gene sequences and the pop
A;Reference number: S60784; MUID:95198537; PMID:7891551
A;Accession: S60802
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 30-89 <WHA>
C;Superfamily: M5 protein
C;Keywords: coiled coil; transmembrane protein

Query Match 100.0%; Score 64; DB 2; Length 539;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
| | | | | | | | | | | | | | | |
Db 390 ASREAKKQVEKALE 403

RESULT 15

A60115
M protein precursor - Streptococcus pyogenes (serotype M12) (fragment)
C;Species: Streptococcus pyogenes
A;Variety: serotype M12
C;Date: 08-Dec-1992 #sequence_revision 08-Dec-1992 #text_change 09-Jul-2004
C;Accession: A40174; A60115; S39887; S61072; S60793
R;Robbins, J.C.; Spanier, J.G.; Jones, S.J.; Simpson, W.J.; Cleary, P.P.
J. Bacteriol. 169, 5633-5640, 1987
A;Title: Streptococcus pyogenes type 12 M protein gene regulation by upstream sequences.
A;Reference number: A40174; MUID:88058777; PMID:2445730
A;Accession: A40174
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-564 <ROB>
A;Cross-references: UNIPROT:P19401; GB:M18269; NID:G153543; PIDN:AAA88573.1; PID:G153544
R;Kraus, W.; Seyer, J.M.; Beachey, E.H.
Infect. Immun. 57, 2457-2461, 1989
A;Title: Vimentin-cross-reactive epitope of type 12 streptococcal M protein.
A;Reference number: A60115; MUID:89307564; PMID:2473037
A;Accession: A60115
A;Molecule type: protein
A;Residues: 42-54 <KRA>
R;Chen, C.; Bormann, N.; Cleary, P.P.
Mol. Gen. Genet. 241, 685-693, 1993
A;Title: VirR and Mry are homologous trans-acting regulators of M protein and C5a peptid
A;Reference number: S39886; MUID:94088463; PMID:7505389
A;Accession: S39887
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-15 <CHE>
R;Whitmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
submitted to the EMBL Data Library, July 1994
A;Description: Noncongruent relationships between variation in emm1 gene sequences and b
A;Reference number: S61072
A;Accession: S61072
A;Molecule type: DNA
A;Residues: 13-111 <WHA>
A;Cross-references: EMBL:U11937; NID:G533551; PIDN:AAA99553.1; PID:G1235807
R;Whitmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
A;Title: Non-congruent relationships between variation in emm gene sequences and the pop
A;Reference number: S60784; MUID:95198537; PMID:7891551
A;Accession: S60793
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 29-89 <WHW>
A;Cross-references: EMBL:U11937
C;Genetics:
A;Gene: emm12
C;Superfamily: M5 protein
C;Keywords: transmembrane protein
F;1-41/Domain: signal sequence #status predicted <SIG>
F;42-564/Product: M protein (fragment) #status predicted <MAT>

Query Match 100.0%; Score 64; DB 2; Length 564;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
| | | | | | | | | | | | | | | |
Db 427 ASREAKKQVEKALE 440

Search completed: August 4, 2005, 09:04:10
Job time : 16.3023 secs

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OM protein - protein search, using sw model

Run on: August 4, 2005, 08:38:38 ; Search time 74.2326 Seconds
(without alignments)
96.576 Million cell updates/sec

Title: US-10-706-275-1

Perfect score: 64
Sequence: 1 ASREAKKQVEKALE 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	100	2 Q54639	Q54639 streptococc
2	64	100.0	100	2 Q54640	Q54640 streptococc
3	64	100.0	100	2 Q93A1	Q93A1 streptococc
4	64	100.0	198	2 Q54832	Q54832 streptococc
5	64	100.0	208	2 P95824	P95824 streptococc
6	64	100.0	208	2 P95825	P95825 streptococc
7	64	100.0	208	2 P95826	P95826 streptococc
8	64	100.0	212	2 Q84DD3	Q84DD3 streptococc
9	64	100.0	237	2 Q6TLR5	Q6TLR5 streptococc
10	64	100.0	251	2 Q6VQ3	Q6VQ3 streptococc
11	64	100.0	279	2 Q8GL87	Q8GL87 streptococc
12	64	100.0	282	2 Q8GLA6	Q8GLA6 streptococc
13	64	100.0	303	2 Q8GL98	Q8GL98 streptococc
14	64	100.0	307	2 Q8GL84	Q8GL84 streptococc
15	64	100.0	314	2 Q8GLB0	Q8GLB0 streptococc
16	64	100.0	317	2 Q8GL92	Q8GL92 streptococc
17	64	100.0	319	2 Q8GLA2	Q8GLA2 streptococc
18	64	100.0	322	2 Q8GLA4	Q8GLA4 streptococc
19	64	100.0	326	2 Q8GL91	Q8GL91 streptococc
20	64	100.0	340	2 Q8GLA1	Q8GLA1 streptococc
21	64	100.0	345	2 Q8GL93	Q8GL93 streptococc
22	64	100.0	347	2 Q93RQ6	Q93RQ6 streptococc
23	64	100.0	362	2 Q8GL90	Q8GL90 streptococc
24	64	100.0	369	2 Q8GL90	Q8GL90 streptococc
25	64	100.0	388	1 PAM_STRPY	P49054 streptococc
26	64	100.0	400	2 Q8N279	Q8N279 streptococc
27	64	100.0	408	2 Q54837	Q54837 streptococc
28	64	100.0	435	2 Q9AMM3	Q9AMM3 streptococc
29	64	100.0	436	2 Q54839	Q54839 streptococc
30	64	100.0	441	2 Q55246	Q55246 streptococc
31	64	100.0	443	2 Q54703	Q54703 streptococc

32	64	100.0	454	2 Q55278	Q55278 streptococc
33	64	100.0	454	2 Q840T7	Q840T7 streptococc
34	64	100.0	457	2 Q54510	Q54510 streptococc
35	64	100.0	455	2 Q83XW0	Q83XW0 streptococc
36	64	100.0	471	2 Q93SL9	Q93SL9 streptococc
37	64	100.0	472	2 Q55279	Q55279 streptococc
38	64	100.0	475	2 Q33631	Q33631 streptococc
39	64	100.0	483	1 M6_STRPY	P08089 streptococc
40	64	100.0	484	2 Q05464	Q05464 streptococc
41	64	100.0	484	2 Q10372	Q10372 streptococc
42	64	100.0	484	2 Q99XV0	Q99XV0 streptococc
43	64	100.0	488	2 Q54830	Q54830 streptococc
44	64	100.0	492	1 M5_STRPS	P02977 streptococc
45	64	100.0	500	2 Q9RHV2	Q9RHV2 streptococc

ALIGNMENTS

RESULT 1

Q54639	PRELIMINARY;	PRT;	100 AA.
AC Q54639;			
DT 01-NOV-1996 (TrEMBLrel. 01, Created)			
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE M1 protein (Fragment).			
OS Streptococcus pyogenes.			
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC Streptococcus.			
OX NCBI_TaxID=1314;			
RN [1]			
RP MEDLINE=95172752; PubMed=7868273;			
RA Musser J.M., Kapur V., Szeto J., Pan X., Swanson D.S., Martin D.R.;			
RT "Genetic diversity and relationships among Streptococcus pyogenes strains expressing serotype M1 protein: recent intercontinental spread of a subclone causing episodes of invasive disease.";			
RL Infect. Immun. 63:994-1003(1995).			
DR EMBL; U20103; AAA85116.1; ..			
DR HSSP; P13276; IEQ1.			
DR GO; GO:0016020; C:membrane; IEA.			
DR InterPro; IPR003345; M_repeat.			
FT Pfam; PF02370; M; 1.			
FT NON_TER 1 100 100			
FT NON_TER 100 100			
SQ SEQUENCE 100 AA; 11243 MW; 9775831PA25DC463 CRC64;			

Query Match 100.0%; Score 64; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14

Db 50 ASREAKKQVEKALE 63

RESULT 2

Q54640	PRELIMINARY;	PRT;	100 AA.
AC Q54640;			
DT 01-NOV-1996 (TrEMBLrel. 01, Created)			
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE M1 protein (Fragment).			
OS Streptococcus pyogenes.			
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC Streptococcus.			
OX NCBI_TaxID=1314;			
RN [1]			
RP SEQUENCE FROM N.A.			
RP MEDLINE=95172752; PubMed=7868273;			
RA Musser J.M., Kapur V., Szeto J., Pan X., Swanson D.S., Martin D.R.;			

RT "Genetic diversity and relationships among Streptococcus pyogenes
 RT strains expressing serotype M1 protein: recent intercontinental spread
 RL of a subclone causing episodes of invasive disease.";
 RL Infect. Immun. 63:994-1003(1995).

DR EMBL; U20104; AAA85117.1; -.
 DR HSSP; P13276; IEQ1.

DR GO; GO:0016020; C:membrane; IEA.

DR InterPro; IPR003345; M_repeat.

DR Pfam; PF02370; M; 1.

FT NON_TER 1

FT NON_TER 100 100

SQ SEQUENCE 100 AA; 11287 MW; 9773331914EDC2D3 CRC64;

Query Match 100.0%; Score 64; DB 2; Length 100;

Best Local Similarity 100.0%; Pred. No. 0.041;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14

|||||

Db 50 ASREAKKQVEKALE 63

RESULT 3

Q9R3A1 PRELIMINARY; PRT; 100 AA.

AC Q9R3A1; 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE M1 protein (Fragment).

OS Streptococcus pyogenes.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=1314;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=95172752; PubMed=7868273;

RA Musser J.M., Kapur V., Sreto J., Pan X., Swanson D.S., Martin D.R.;

RT "Genetic diversity and relationships among Streptococcus pyogenes

RT strains expressing serotype M1 protein: recent intercontinental spread

RT of a subclone causing episodes of invasive disease.";

RL Infect. Immun. 63:994-1003(1995).

DR EMBL; U20102; AAA85115.1; -.

DR HSSP; P13276; IEQ1.

DR GO; GO:0016020; C:membrane; IEA.

DR InterPro; IPR003345; M_repeat.

DR Pfam; PF02370; M; 1.

FT NON_TER 1

FT NON_TER 100 100

SQ SEQUENCE 100 AA; 11345 MW; 9773331C00EDC2D3 CRC64;

Query Match 100.0%; Score 64; DB 2; Length 100;

Best Local Similarity 100.0%; Pred. No. 0.041;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14

|||||

Db 50 ASREAKKQVEKALE 63

RESULT 4

Q54832 PRELIMINARY; PRT; 198 AA.

AC Q54832; 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE M protein (Fragment).

GN Name=emm3;

OS Streptococcus pyogenes.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=1314;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93062420; PubMed=1435517;

RA Podbielski A., Baird R., Kaufhold A.;

RT "The group A streptococcal M-type 3 protein gene exhibits a C terminus

RT typical for class I M proteins.";

RL Med. Microbiol. Immunol. 181:209-213(1992).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=93062420; PubMed=1435517;

RA Podbielski A., Kaufhold A.;

RT Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.

RL -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by

CC an amide bond (By similarity).

DR EMBL; X66816; CAA47295.1; -.

DR GO; GO:0009986; C:cell surface; IEA.

DR GO; GO:0005618; C:cell wall; IEA.

DR GO; GO:0016020; C:membrane; IEA.

DR InterPro; IPR001899; Gram_pos_anchor.

DR InterPro; IPR003345; M_repeat.

DR Pfam; PF00746; Gram_pos_anchor; 1.

DR PRINTS; PR00015; GPOSANCHOR.

DR TIGRPFAM; TIGR01167; LPXTG anchor; 1.

DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.

DR Cell wall; Peptidoglycan-anchor.

FT NON_TER 1

FT NON_TER 198 AA; 21550 MW; A738888D947155D5 CRC64;

SQ SEQUENCE 100.0%; Score 64; DB 2; Length 198;

Best Local Similarity 100.0%; Pred. No. 0.078;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14

|||||

Db 49 ASREAKKQVEKALE 62

RESULT 5

P95824 PRELIMINARY; PRT; 208 AA.

AC P95824; 01-MAY-1997 (TrEMBLrel. 03, Created)

DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE M protein (Fragment).

OS Streptococcus pyogenes.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=1314;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=M nontypeable group A;

RA Brandt E.R., Good M.F.;

RT Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.

RL -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by

CC an amide bond (By similarity).

DR EMBL; U65899; AAB40640.1; -.

DR GO; GO:0009986; C:cell surface; IEA.

DR GO; GO:0005618; C:cell wall; IEA.

DR GO; GO:0016020; C:membrane; IEA.

DR InterPro; IPR001899; Gram_pos_anchor.

DR InterPro; IPR003345; M_repeat.

DR Pfam; PF00746; Gram_pos_anchor; 1.

DR PRINTS; PR00015; GPOSANCHOR.

DR TIGRPFAM; TIGR01167; LPXTG anchor; 1.

DR PROSITE; PSS0847; GRAM_POS_ANCHORING; 1.

DR Cell wall; Peptidoglycan-anchor.

FT NON_TER 1

FT NON_TER 208 208

```
SQ SEQUENCE 208 AA; 22695 MW; 013FBBAB0A97FF42 CRC64;
Query Match 100.0%; Score 64; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
Db 59 ASREAKKQVEKALE 72

RESULT 6
P95825 ID P95825 PRELIMINARY; PRT; 208 AA.
AC P95825;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE M protein (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=reference;
RA Brandt E.R., Good M.F.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (by similarity).
DR EMBL; U65900; AAB40641.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR PRINTS; PR00015; GPOSANCHOR.
DR TIGRFAMs; TIGR01167; LPXTG anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
FT NON_TER 1
FT CHAIN 23 >212 M protein.
FT NON_TER 212 212
SQ SEQUENCE 208 AA; 22817 MW; 790342752FB17720 CRC64;
Query Match 100.0%; Score 64; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
Db 59 ASREAKKQVEKALE 72

RESULT 7
P95826 ID P95826 PRELIMINARY; PRT; 208 AA.
AC P95826;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE M protein (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RHD152-;
RA Brandt E.R., Good M.F.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
```

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an amide bond (by similarity).
DR EMBL; U66005; AAB40642.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR PRINTS; PR00015; GPOSANCHOR.
DR TIGRFAMs; TIGR01167; LPXTG anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
FT NON_TER 1
FT CHAIN 23 >212 M protein.
FT NON_TER 212 212
SQ SEQUENCE 208 AA; 22565 MW; 79972A987324729B CRC64;
Query Match 100.0%; Score 64; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
Db 59 ASREAKKQVEKALE 72

RESULT 8
Q84DD3 ID Q84DD3 PRELIMINARY; PRT; 212 AA.
AC Q84DD3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE M protein (Fragment).
GN Name=emm;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RA Beall B.W.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY225412; AAO67526.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF02370; M; 2.
DR NON_TER 1
FT CHAIN 23 >212 M protein.
FT NON_TER 212 212
SQ SEQUENCE 212 AA; 24116 MW; 0A7EB56F0FCAEF26 CRC64;
Query Match 100.0%; Score 64; DB 2; Length 212;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
Db 197 ASREAKKQVEKALE 210

RESULT 9
Q6TLR5 ID Q6TLR5 PRELIMINARY; PRT; 237 AA.
AC Q6TLR5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE M protein (Fragment).
GN Name=emm;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
```

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OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NS241;
RX MEDLINE=22894607; PubMed=14532198;
RA Moses A.E., Hidalgo-Grass C., Dan-Goor M., Jaffe J., Shetzigovsky I.,
RA Ravins M., Korenman Z., Cohen-Poradosu R., Nir-Paz R.;
RT "emm typing of M nontypeable invasive group A streptococcal isolates
  in Israel.";
RL J. Clin. Microbiol. 41:4655-4659(2003).
DR EMBL; AY394538; AAQ94530.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF02370; M; 1.
FT NON_TER 1
FT NON_TER 237
SQ SEQUENCE 237 AA; 27027 MW; 47CFF315DD4EB5F2 CRC64;

Query Match 100.0%; Score 64; DB 2; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
   |||||
Db 192 ASREAKKQVEKALE 205

RESULT 10
Q6V9Q3 PRELIMINARY; PRT; 251 AA.
AC Q6V9Q3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE M protein (Fragment).
GN Name=emm;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JS8;
RA Moses A.E., Hidalgo-Grass C., Dan-Goor M., Jaffe J., Shetzigovsky I.,
RA Ravins M., Korenman Z., Cohen-Poradosu R., Nir-Paz R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY346386; AAQ73206.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF02370; M; 1.
FT NON_TER 1
FT NON_TER 251
SQ SEQUENCE 251 AA; 28938 MW; 2A66602AAAG37D11 CRC64;

Query Match 100.0%; Score 64; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
   |||||
Db 221 ASREAKKQVEKALE 234

RESULT 11
Q8GL87 PRELIMINARY; PRT; 279 AA.
AC Q8GL87;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE M protein (Fragment).
GN Name=emm;
OS Streptococcus pyogenes.

```

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OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RA Dyall-Smith M.L., Krejany S., Sriprakash K.S., Delvecchio A.,
RA McMillan D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY139420; AAN64693.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF02370; M; 2.
FT NON_TER 1
FT NON_TER 279
SQ SEQUENCE 279 AA; 31224 MW; 16A600455B5C3A0 CRC64;

Query Match 100.0%; Score 64; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
   |||||
Db 224 ASREAKKQVEKALE 237

RESULT 12
Q8GLA6 PRELIMINARY; PRT; 282 AA.
AC Q8GLA6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE M protein (Fragment).
GN Name=emm;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RA Dyall-Smith M.L., Krejany S., Sriprakash K.S., Delvecchio A.,
RA McMillan D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY139403; AAN64674.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF02370; M; 1.
FT NON_TER 1
FT NON_TER 282
SQ SEQUENCE 282 AA; 32157 MW; 5C799B0AA4323541 CRC64;

Query Match 100.0%; Score 64; DB 2; Length 282;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASREAKKQVEKALE 14
   |||||
Db 226 ASREAKKQVEKALE 239

RESULT 13
Q8GL98 PRELIMINARY; PRT; 303 AA.
AC Q8GL98;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE M protein (Fragment).
GN Name=emm;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;

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RN SEQUENCE FROM N.A.
 RP Dyall-Smith M.L., Krejany S., Sriprakash K.S., Delvecchio A.,
 RA McMillan D.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY139409; AAN64682.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR003345; M_repeat.
 DR Pfam; PF02370; M; 2.
 FT NON_TER 1 1
 FT NON_TER 303 303
 SQ SEQUENCE 303 AA; 34562 MW; F76F37540E16CD1B CRC64;

Query Match 100.0%; Score 64; DB 2; Length 303;
 Best Local Similarity 100.0%; Pred. NO. 0.12;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
 |||||
 Db 246 ASREAKKQVEKALE 259

RESULT 14

Q8GL84 Q8GL84 PRELIMINARY; PRT; 307 AA.
 AC Q8GL84;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE M protein (Fragment).
 GN Name=emm;
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dyall-Smith M.L., Krejany S., Sriprakash K.S., Delvecchio A.,
 RA McMillan D.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY139423; AAN64696.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR003345; M_repeat.
 DR Pfam; PF02370; M; 2.
 FT NON_TER 1 1
 FT NON_TER 307 307
 SQ SEQUENCE 307 AA; 34955 MW; 2268229938566E0E CRC64;

Query Match 100.0%; Score 64; DB 2; Length 307;
 Best Local Similarity 100.0%; Pred. NO. 0.12;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
 |||||
 Db 251 ASREAKKQVEKALE 264

RESULT 15

Q8GLB0 Q8GLB0 PRELIMINARY; PRT; 314 AA.
 AC Q8GLB0;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE M protein (Fragment).
 GN Name=emm;
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dyall-Smith M.L., Krejany S., Sriprakash K.S., Delvecchio A.,

RA McMillan D.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY139397; AAN64670.1; -;
 DR HSP; P04268; IIC2
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR003345; M_repeat.
 DR Pfam; PF02370; M; 2.
 FT NON_TER 1 1
 FT NON_TER 314 314
 SQ SEQUENCE 314 AA; 35613 MW; 66173BEEB74C9EFC CRC64;

Query Match 100.0%; Score 64; DB 2; Length 314;
 Best Local Similarity 100.0%; Pred. NO. 0.12;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
 |||||
 Db 259 ASREAKKQVEKALE 272

Search completed: August 4, 2005, 09:03:17
 Job time : 76.2326 secs

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OM protein - protein search, using sw model

Run on: August 4, 2005, 08:37:33 ; Search time 163.209 Seconds
(without alignments)
68.722 Million cell updates/sec

Title: US-10-706-275-2

Perfect score: 137
Sequence: 1 KQAEKVKASREAKQVKALEQLEDKVK 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 segs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	137	100.0	29	8	ADK00565 Immunogen
2	137	100.0	45	8	ADK00571 Immunogen
3	137	100.0	46	8	ADK00569 Immunogen
4	137	100.0	46	8	ADK00572 Immunogen
5	137	100.0	47	8	ADK00570 Immunogen
6	125	91.2	28	2	AAW04353 Chimaeric
7	123	89.8	28	2	AAW04354 Chimaeric
8	116	84.7	28	2	AAW04355 Chimaeric
9	110	80.3	28	2	AAW04352 Chimaeric
10	96	70.1	28	2	AAW04351 Chimaeric
11	81	59.1	28	2	AAW04350 Chimaeric
12	78	56.9	28	2	AAR97454 Chimaeric
13	72	52.6	234	2	AAR10221 Streptoco
14	72	52.6	281	2	AAR20128 Sequence
15	72	52.6	441	1	AAP90955 M6 strept
16	72	52.6	441	2	AAR41780 Streptoco
17	72	52.6	441	7	ADG62862 Streptoco
18	72	52.6	483	2	AAW08927 Type-6 M-
19	72	52.6	484	5	ABP30015 Streptoco
20	72	52.6	484	8	ADP30115 Streptoco
21	71	51.8	28	2	AAR97396 (GCN4)4 a
22	71	51.8	236	3	AAB03118 C-terminu
23	71	51.8	254	2	AAR50228 Sequence
24	71	51.8	284	2	AAR50229 Sequence
25	71	51.8	305	2	AAR50996 Recombina

26	71	51.8	305	3	AAB03117 S. pyogen
27	71	51.8	539	8	ADP49327 S. pyogen
28	68.5	50.0	28	2	AAR97453 Chimaeric
29	67	48.9	29	2	AAR97439 Chimaeric
30	67	48.9	389	6	ABU39221 Protein e
31	66	48.2	284	8	ADL99394 Nanostruc
32	65.5	47.8	28	2	AAW04349 Chimaeric
33	65	47.4	29	2	AAR97461 Chimaeric
34	64	46.7	20	2	AAR43343 B cell ep
35	64	46.7	20	2	AAR97390 Streptoco
36	64	46.7	20	2	AAW69281 Streptoco
37	64	46.7	29	2	AAR97460 Chimaeric
38	64	46.7	37	6	ADA16009 Synthetic
39	64	46.7	72	2	AAR32701 SSP-egg34
40	64	46.7	361	7	ADF05105 Bacterial
41	63.5	46.4	65	7	ADG62863 Streptoco
42	63	46.0	29	2	AAR97466 Chimaeric
43	63	46.0	29	2	AAR97442 Chimaeric
44	63	46.0	107	2	AAR32705 SSP-534 p
45	63	46.0	107	2	AAR78265 Synthetic

ALIGNMENTS

RESULT 1

ADK00565
ID ADK00565 standard; peptide; 29 AA.

XX ADK00565;

XX 06-MAY-2004 (first entry)

XX Immunogenic lipopeptide of the invention #101.

XX T helper cell epitope; B cell epitope; Antibacterial; Antiulcer;

KW Antiinfertility; Vaccine; antibody.

XX Synthetic.

XX WO2004014956-A1.

XX 19-FEB-2004.

XX 12-AUG-2003; 2003WO-AU001018.

XX 12-AUG-2002; 2002US-0402838P.

XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.

XX Jackson D, Zeng W;

XX WPI; 2004-238735/22.

XX Novel lipopeptide comprising polypeptide having amino acid sequence of T
PT helper cell epitope and B cell epitope, conjugated to lipid moieties,
PT useful for eliciting immune response against group A Streptococcus
PT antigen.

XX Claim 29; SEQ ID NO 101; 194pp; English.

XX The present invention relates to a lipopeptide comprising polypeptide
conjugated to lipid moieties, where polypeptide contains amino acid
sequence of T helper cell epitope and B cell epitope, where amino acid
sequences are different, and internal lysine residues or internal lysine
analog residues for covalent attachment of each of lipid moieties through
CC segr; amino group or terminal side chain group of lysine or lysine
CC analog. The peptides are useful in eliciting the production of antibody
CC against an antigenic B cell epitope in a subject, and are useful for
CC antibody production, synthetic vaccine production, diagnostic method
CC employing antibodies and antibody ligands and immunotherapy for
CC veterinary and human medicine. The method efficiently elicits the
CC production of antibody against antigenic B cell epitope. The present

CC sequence represents a novel immunogenic lipopeptide comprising T helper
 CC and B cell epitopes.

XX Sequence 29 AA;

Query Match 100.0%; Score 137; DB 8; Length 29;
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOAEDKVKASREAKKQVEKALEQLEDKVK 29
 |||||

DB 1 KOAEDKVKASREAKKQVEKALEQLEDKVK 29
 |||||

RESULT 2

ADK00571

ID ADK00571 standard; peptide; 45 AA.

XX AC ADK00571;

XX DT 06-MAY-2004 (first entry)

XX Immunogenic lipopeptide of the invention #107.

XX T helper cell epitope; B cell epitope; Antibacterial; Antiulcer;

KW Antinfertility; Vaccine; antibody.

XX OS Synthetic.

XX PN WO2004014956-A1.

XX PD 19-FEB-2004.

XX PF 12-AUG-2003; 2003WO-AU001018.

XX PR 12-AUG-2002; 2002US-0402838P.

XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.

XX PI Jackson D, Zeng W;

XX DR WPI; 2004-238735/22.

XX Novel lipopeptide comprising polypeptide having amino acid sequence of T
 PT helper cell epitope and B cell epitope, conjugated to lipid moieties,
 PT useful for eliciting immune response against group A Streptococcus
 PT antigen.

XX PS Claim 39; SEQ ID NO 107; 194pp; English.

CC The present invention relates to a lipopeptide comprising polypeptide
 CC conjugated to lipid moieties, where polypeptide contains amino acid
 CC sequence of T helper cell epitope and B cell epitope, where amino acid
 CC sequences are different, and internal lysine residues or internal lysine
 CC analog residues for covalent attachment of each of lipid moieties through
 CC legr; amino group or terminal side chain group of lysine or lysine
 CC analog. The peptides are useful in eliciting the production of antibody
 CC against an antigenic B cell epitope in a subject, and are useful for
 CC antibody production, synthetic vaccine production, diagnostic method
 CC employing antibodies and antibody ligands and immunotherapy for
 CC veterinary and human medicine. The method efficiently elicits the
 CC production of antibody against antigenic B cell epitope. The present
 CC sequence represents a novel immunogenic lipopeptide comprising T helper
 CC and B cell epitopes.

XX Sequence 45 AA;

Query Match 100.0%; Score 137; DB 8; Length 45;
 Best Local Similarity 100.0%; Pred. No. 1.8e-09;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOAEDKVKASREAKKQVEKALEQLEDKVK 29
 |||||

DB 17 KOAEDKVKASREAKKQVEKALEQLEDKVK 45

RESULT 3

ADK00569

ID ADK00569 standard; peptide; 46 AA.

XX AC ADK00569;

XX DT 06-MAY-2004 (first entry)

XX Immunogenic lipopeptide of the invention #105.

XX T helper cell epitope; B cell epitope; Antibacterial; Antiulcer;

KW Antinfertility; Vaccine; antibody.

XX OS Synthetic.

XX PN WO2004014956-A1.

XX PD 19-FEB-2004.

XX PF 12-AUG-2003; 2003WO-AU001018.

XX PR 12-AUG-2002; 2002US-0402838P.

XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.

XX PI Jackson D, Zeng W;

XX DR WPI; 2004-238735/22.

XX Novel lipopeptide comprising polypeptide having amino acid sequence of T
 PT helper cell epitope and B cell epitope, conjugated to lipid moieties,
 PT useful for eliciting immune response against group A Streptococcus
 PT antigen.

XX PS Claim 39; SEQ ID NO 105; 194pp; English.

XX The present invention relates to a lipopeptide comprising polypeptide
 CC conjugated to lipid moieties, where polypeptide contains amino acid
 CC sequence of T helper cell epitope and B cell epitope, where amino acid
 CC sequences are different, and internal lysine residues or internal lysine
 CC analog residues for covalent attachment of each of lipid moieties through
 CC legr; amino group or terminal side chain group of lysine or lysine
 CC analog. The peptides are useful in eliciting the production of antibody
 CC against an antigenic B cell epitope in a subject, and are useful for
 CC antibody production, synthetic vaccine production, diagnostic method
 CC employing antibodies and antibody ligands and immunotherapy for
 CC veterinary and human medicine. The method efficiently elicits the
 CC production of antibody against antigenic B cell epitope. The present
 CC sequence represents a novel immunogenic lipopeptide comprising T helper
 CC and B cell epitopes.

XX Sequence 46 AA;

Query Match 100.0%; Score 137; DB 8; Length 46;
 Best Local Similarity 100.0%; Pred. No. 1.9e-09;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOAEDKVKASREAKKQVEKALEQLEDKVK 29
 |||||

DB 18 KOAEDKVKASREAKKQVEKALEQLEDKVK 46
 |||||

RESULT 4

ADK00572

ID ADK00572 standard; peptide; 46 AA.

XX AC ADK00572;

XX DT 06-MAY-2004 (first entry)

DE Immunogenic lipopeptide of the invention #108.
 XX T helper cell epitope; B cell epitope; Antibacterial; Antiulcer;
 KW Antiinfertility; Vaccine; antibody.
 XX Synthetic.
 OS
 PN WO2004014956-A1.
 XX
 PD 19-FEB-2004.
 XX
 XX 12-AUG-2003; 2003WO-AU001018.
 PF
 XX 12-AUG-2002; 2002US-0402838P.
 PR
 XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 PA Jackson D, Zeng W;
 XX WPI; 2004-238735/22.
 DR
 XX Novel lipopeptide comprising polypeptide having amino acid sequence of T
 PT helper cell epitope and B cell epitope, conjugated to lipid moieties,
 PT useful for eliciting immune response against group A Streptococcus
 PT antigen.
 CC
 XX Claim 39; SEQ ID NO 108; 194pp; English.
 PS
 XX The present invention relates to a lipopeptide comprising polypeptide
 CC conjugated to lipid moieties, where polypeptide contains amino acid
 CC sequence of T helper cell epitope and B cell epitope, where amino acid
 CC sequences are different, and internal lysine residues or internal lysine
 CC analog residues for covalent attachment of each of lipid moieties through
 CC a sugar; amino group or terminal side chain group of lysine or lysine
 CC analog. The peptides are useful in eliciting the production of antibody
 CC against an antigenic B cell epitope in a subject, and are useful for
 CC antibody production, synthetic vaccine production, diagnostic method
 CC employing antibodies and antibody ligands and immunotherapy for
 CC veterinary and human medicine. The method efficiently elicits the
 CC production of antibody against antigenic B cell epitope. The present
 CC sequence represents a novel immunogenic lipopeptide comprising T helper
 CC and B cell epitopes.
 XX
 SQ Sequence 46 AA;
 Query Match 100.0%; Score 137; DB 8; Length 46;
 Best Local Similarity 100.0%; Pred. No. 1.9e-09;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KOAEDKVKASREAKKQVEKALEQLEDKVK 29
 DB 18 KOAEDKVKASREAKKQVEKALEQLEDKVK 46
 RESULT 5
 ADK00570
 ID ADK00570 standard; peptide; 47 AA.
 AC
 XX ADK00570;
 XX
 XX 06-MAY-2004 (first entry)
 DT
 XX Immunogenic lipopeptide of the invention #106.
 DE
 XX T helper cell epitope; B cell epitope; Antibacterial; Antiulcer;
 KW Antiinfertility; Vaccine; antibody.
 XX Synthetic.
 OS
 XX WO2004014956-A1.
 PN
 XX 19-FEB-2004.
 PD
 XX

PF 12-AUG-2003; 2003WO-AU001018.
 XX
 PR 12-AUG-2002; 2002US-0402838P.
 XX
 PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 XX Jackson D, Zeng W;
 XX WPI; 2004-238735/22.
 DR
 XX Novel lipopeptide comprising polypeptide having amino acid sequence of T
 PT helper cell epitope and B cell epitope, conjugated to lipid moieties,
 PT useful for eliciting immune response against group A Streptococcus
 PT antigen.
 CC
 XX Claim 39; SEQ ID NO 106; 194pp; English.
 PS
 XX The present invention relates to a lipopeptide comprising polypeptide
 CC conjugated to lipid moieties, where polypeptide contains amino acid
 CC sequence of T helper cell epitope and B cell epitope, where amino acid
 CC sequences are different, and internal lysine residues or internal lysine
 CC analog residues for covalent attachment of each of lipid moieties through
 CC a sugar; amino group or terminal side chain group of lysine or lysine
 CC analog. The peptides are useful in eliciting the production of antibody
 CC against an antigenic B cell epitope in a subject, and are useful for
 CC antibody production, synthetic vaccine production, diagnostic method
 CC employing antibodies and antibody ligands and immunotherapy for
 CC veterinary and human medicine. The method efficiently elicits the
 CC production of antibody against antigenic B cell epitope. The present
 CC sequence represents a novel immunogenic lipopeptide comprising T helper
 CC and B cell epitopes.
 XX
 SQ Sequence 47 AA;
 Query Match 100.0%; Score 137; DB 8; Length 47;
 Best Local Similarity 100.0%; Pred. No. 1.9e-09;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KOAEDKVKASREAKKQVEKALEQLEDKVK 29
 DB 19 KOAEDKVKASREAKKQVEKALEQLEDKVK 47
 RESULT 6
 AAW04353
 ID AAW04353 standard; protein; 28 AA.
 XX
 AC AAW04353;
 XX
 DT 02-DEC-1996 (first entry)
 DT
 XX Chimaeric peptide (J7) contg. Streptococcal M protein peptide p145.
 DE
 XX Streptococcal; M protein; peptide; p145; chimaeric; chimeric; B-cell;
 KW conformational epitope; alpha-helix; GCN4; leucine zipper; detection;
 KW mapping; opsonic antibody; vaccine; group A Streptococci; immunotherapy;
 KW diagnosis.
 XX
 OS Synthetic.
 OS
 XX Key Location/Qualifiers
 FH 15..26
 FT Peptide /note= "p145 conformational B-cell epitope"
 FT
 XX WO9611944-A1.
 PN
 XX 25-APR-1996.
 PD
 XX 16-OCT-1995; 95WO-AU000681.
 PF
 XX 14-OCT-1994; 94AU-00008851.
 PR
 XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 PA

PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (UYME) UNIV MELBOURNE.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.
 PA (CSLC-) CSL LTD.
 XX
 PI Cooper JA, Relf WA, Good MF, Saul AJ;
 XX
 DR WPI; 1996-221939/22.
 XX
 XX New chimeric peptide(s) including a conformational epitope - inserted
 PT into a peptide having similar native conformation, useful in vaccines and
 PT for determin. of minimal epitope(s) or for mapping amphipathic helices.
 XX
 XX Example 12; Fig 1C; 99pp; English.
 XX
 CC The present peptide is a chimaeric peptide (CP) contg. the Streptococcal
 CC M protein peptide p145 (Pruksakorn et al, J. Immunol. 149: 2729-2735
 CC (1992)). The CP comprises a B-cell conformational epitope from within
 CC p145, inserted into a 2nd peptide, pref. an alpha-helical coil based on
 CC the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide has a similar
 CC conformation, enabling the epitope to be presented in an immunologically
 CC active conformation. The CP can be used in a novel detection/mapping
 CC process, e.g. to determine the min. epitope required to induce opsonic
 CC antibodies (Ab), and in vaccines against gp. A Streptococci. Ab raised
 CC against the CP can be used for immunotherapy and diagnosis, while the CP
 CC can be used diagnostically to detect Ab. The reactivity of the present
 CC peptide to the anti-p145 mouse serum 11/1(8) given as a mean absorbance
 CC value at 405 nm was ca. 0.2, compared to ca. 1.8 for p145
 XX
 SQ Sequence 28 AA;
 Query Match 91.2%; Score 125; DB 2; Length 28;
 Best Local Similarity 92.9%; Pred. No. 3e-08;
 Matches 26; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQAEKVKASREAKQVEKALEQLEDKVK 28
 Db |||||||||||||||||||:|||||
 1 KQAEKVKASREAKQVEKALEQLEDKVK 28
 RESULT 7
 AAW04354
 ID AAW04354 standard; protein; 28 AA.
 XX
 AC AAW04354;
 XX
 DT 02-DEC-1996 (first entry)
 XX
 DE Chimaeric peptide (J9) contg. Streptococcal M protein peptide p145.
 XX
 KW Streptococcal; M protein; peptide; p145; chimaeric; chimeric; B-cell;
 KW conformational epitope; alpha-helix; GCN4; leucine zipper; detection;
 KW mapping; opsonic antibody; vaccine; group A Streptococci; immunotherapy;
 KW diagnosis.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 16..27
 FT /note= "p145 conformational B-cell epitope"
 FT
 XX WO9611944-A1.
 XX
 PD 25-APR-1996.
 XX
 PF 16-OCT-1995; 95WO-AU000681.
 XX
 PR 14-OCT-1994; 94AU-00008851.
 XX
 XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (UYME) UNIV MELBOURNE.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.
 PA (CSLC-) CSL LTD.

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.
 PA (CSLC-) CSL LTD.
 XX
 PI Cooper JA, Relf WA, Good MF, Saul AJ;
 XX
 DR WPI; 1996-221939/22.
 XX
 XX New chimeric peptide(s) including a conformational epitope - inserted
 PT into a peptide having similar native conformation, useful in vaccines and
 PT for determin. of minimal epitope(s) or for mapping amphipathic helices.
 XX
 XX Example 12; Fig 1C; 99pp; English.
 XX
 CC The present peptide is a chimaeric peptide (CP) contg. the Streptococcal
 CC M protein peptide p145 (Pruksakorn et al, J. Immunol. 149: 2729-2735
 CC (1992)). The CP comprises a B-cell conformational epitope from within
 CC p145, inserted into a 2nd peptide, pref. an alpha-helical coil based on
 CC the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide has a similar
 CC conformation, enabling the epitope to be presented in an immunologically
 CC active conformation. The CP can be used in a novel detection/mapping
 CC process, e.g. to determine the min. epitope required to induce opsonic
 CC antibodies (Ab), and in vaccines against gp. A Streptococci. Ab raised
 CC against the CP can be used for immunotherapy and diagnosis, while the CP
 CC can be used diagnostically to detect Ab. The reactivity of the present
 CC peptide to the anti-p145 mouse serum 11/1(8) given as a mean absorbance
 CC value at 405 nm was ca. 0.2, compared to ca. 1.8 for p145
 XX
 SQ Sequence 28 AA;
 Query Match 89.8%; Score 123; DB 2; Length 28;
 Best Local Similarity 92.9%; Pred. No. 5.3e-08;
 Matches 26; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 QAEKVKASREAKQVEKALEQLEDKVK 29
 Db |||||||||||||||||||:|||||
 1 QAEKVKASREAKQVEKALEQLEDKVK 28
 RESULT 8
 AAW04355
 ID AAW04355 standard; protein; 28 AA.
 XX
 AC AAW04355;
 XX
 DT 02-DEC-1996 (first entry)
 XX
 DE Chimaeric peptide (J9) contg. Streptococcal M protein peptide p145.
 XX
 KW Streptococcal; M protein; peptide; p145; chimaeric; chimeric; B-cell;
 KW conformational epitope; alpha-helix; GCN4; leucine zipper; detection;
 KW mapping; opsonic antibody; vaccine; group A Streptococci; immunotherapy;
 KW diagnosis.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 17..28
 FT /note= "p145 conformational B-cell epitope"
 FT
 XX WO9611944-A1.
 XX
 PD 25-APR-1996.
 XX
 PF 16-OCT-1995; 95WO-AU000681.
 XX
 PR 14-OCT-1994; 94AU-00008851.
 XX
 XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (UYME) UNIV MELBOURNE.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.

PA (CSLC-) CSL LTD.
 XX
 PI Cooper JA, Relf WA, Good MF, Saul AJ;
 XX WPI; 1996-221939/22.
 XX
 XX New chimeric peptide(s) including a conformational epitope - inserted
 PT into a peptide having similar native conformation, useful in vaccines and
 PT for determin. of minimal epitope(s) or for mapping amphipathic helices.
 XX
 XX Example 12; Fig 1C; 99pp; English.
 XX
 CC The present peptide is a chimaeric peptide (CP) contg. the Streptococcal
 CC M protein peptide p145 (Prukaorn et al, J. Immunol. 149: 2729-2735
 CC (1992)). The CP comprises a B-cell conformational epitope from within
 CC p145, inserted into a 2nd peptide, pref. an alpha-helical coil based on
 CC the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide has a similar
 CC conformation, enabling the epitope to be presented in an immunologically
 CC active conformation. The CP can be used in a novel detection/mapping
 CC process, e.g. to determine the min. epitope required to induce opsonic
 CC antibodies (Ab), and in vaccines against gp. A Streptococci. Ab raised
 CC against the CP can be used for immunotherapy and diagnosis, while the CP
 CC can be used diagnostically to detect Ab. The reactivity of the present
 CC peptide to the anti-p145 mouse serum 11/1(8) given as a mean absorbance
 CC value at 405 nm was ca. 0.2, compared to ca. 1.8 for p145
 XX
 XX Sequence 28 AA;

Query Match 84.7%; Score 116; DB 2; Length 28;
 Best Local Similarity 92.6%; Pred. No. 3.7e-07;
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 AEDKVKASREAKQVEKALEQLEDK 29
 ||||| ||||| ||||| ||||| |||||
 DB 1 AEDKVKQLEAKQVEKALEQLEDK 27

RESULT 9
 AA04352
 ID AA04352 standard; protein; 28 AA.
 AC AA04352;
 XX
 XX 02-DEC-1996 (first entry)
 XX
 XX Chimaeric peptide (J6) contg. Streptococcal M protein peptide p145.
 XX Streptococcal; M protein; peptide; p145; chimaeric; chimeric; B-cell;
 XX conformational epitope; alpha-helix; GCN4; leucine zipper; detection;
 XX mapping; opsonic antibody; vaccine; group A Streptococci; immunotherapy;
 XX diagnosis.
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Peptide 14..25
 FT /note= "p145 conformational B-cell epitope"
 XX
 XX WO9611944-A1.
 XX
 XX 25-APR-1996.
 XX
 XX 16-OCT-1995; 95WO-AU000681.
 XX
 XX 14-OCT-1994; 94AU-00008851.
 XX
 XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX (UYME) UNIV MELBOURNE.
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 XX (BIOT-) BIOTECH AUSTRALIA PTY LTD.
 XX (CSLC-) CSL LTD.
 XX

PI Cooper JA, Relf WA, Good MF, Saul AJ;
 XX WPI; 1996-221939/22.
 XX
 XX New chimeric peptide(s) including a conformational epitope - inserted
 PT into a peptide having similar native conformation, useful in vaccines and
 PT for determin. of minimal epitope(s) or for mapping amphipathic helices.
 XX
 XX Example 12; Fig 1C; 99pp; English.
 XX
 CC The present peptide is a chimaeric peptide (CP) contg. the Streptococcal
 CC M protein peptide p145 (Prukaorn et al, J. Immunol. 149: 2729-2735
 CC (1992)). The CP comprises a B-cell conformational epitope from within
 CC p145, inserted into a 2nd peptide, pref. an alpha-helical coil based on
 CC the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide has a similar
 CC conformation, enabling the epitope to be presented in an immunologically
 CC active conformation. The CP can be used in a novel detection/mapping
 CC process, e.g. to determine the min. epitope required to induce opsonic
 CC antibodies (Ab), and in vaccines against gp. A Streptococci. Ab raised
 CC against the CP can be used for immunotherapy and diagnosis, while the CP
 CC can be used diagnostically to detect Ab. The reactivity of the present
 CC peptide to the anti-p145 mouse serum 11/1(8) given as a mean absorbance
 CC value at 405 nm was ca. 0.2, compared to ca. 1.8 for p145
 XX
 XX Sequence 28 AA;

Query Match 80.3%; Score 110; DB 2; Length 28;
 Best Local Similarity 85.2%; Pred. No. 2e-06;
 Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KQAEKVKASREAKQVEKALEQLEDK 27
 ||||| ||||| ||||| ||||| |||||
 DB 2 KQAEKVKDASREAKQVEKVKQLEDK 28

RESULT 10
 AA04351
 ID AA04351 standard; protein; 28 AA.
 AC AA04351;
 XX
 XX 02-DEC-1996 (first entry)
 XX
 XX Chimaeric peptide (J5) contg. Streptococcal M protein peptide p145.
 XX Streptococcal; M protein; peptide; p145; chimaeric; chimeric; B-cell;
 XX conformational epitope; alpha-helix; GCN4; leucine zipper; detection;
 XX mapping; opsonic antibody; vaccine; group A Streptococci; immunotherapy;
 XX diagnosis.
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Peptide 13..24
 FT /note= "p145 conformational B-cell epitope"
 XX
 XX WO9611944-A1.
 XX
 XX 25-APR-1996.
 XX
 XX 16-OCT-1995; 95WO-AU000681.
 XX
 XX 14-OCT-1994; 94AU-00008851.
 XX
 XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX (UYME) UNIV MELBOURNE.
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 XX (BIOT-) BIOTECH AUSTRALIA PTY LTD.
 XX (CSLC-) CSL LTD.
 XX
 XX Cooper JA, Relf WA, Good MF, Saul AJ;
 XX

CC 15 paramyosin peptide. The CP comprises a B-cell conformational epitope
 CC from within unc-15, inserted into a 2nd peptide, pref. an alpha-helical
 CC coil based on the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide
 CC has a similar conformation, enabling the epitope to be presented in an
 CC immunologically active conformation. The CP can be used in a novel
 CC detection/mapping process, e.g. to determine the min. epitope required to
 CC induce opsonic antibodies (Ab), and in vaccines against *C. elegans*. Ab
 CC raised against the CP can be used for immunotherapy and diagnosis, while
 CC the CP can be used diagnostically to detect Ab

XX SQ Sequence 28 AA;

Query Match 56.9%; Score 78; DB 2; Length 28;
 Best Local Similarity 64.0%; Pred. No. 0.015;
 Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 KQAEKVKASREAKQVEKALEOLE 25
 Db 4 KQAEEDLDASREAKQLQDKVKQLE 28

RESULT 13

AAR10221
 ID AAR10221 standard; protein; 234 AA.

XX AC AAR10221;

XX DT 25-MAR-2003 (revised)

XX DT 26-MAR-1991 (first entry)

XX DE Streptococcal M6' protein.

XX KW Streptococcal M protein; M'6 protein; vaccinia virus; fowlpox virus;
 XX KW poxviridae vaccine; streptococcal pharyngitis.

XX OS Streptococcus sp.

XX PN WO9015872-A.

XX PD 27-DEC-1990.

XX PF 21-JUN-1989; 89US-00369118.

XX PR 21-JUN-1989; 89US-00369118.

XX PR 19-JUN-1990; 90US-00540586.

XX PA (UYRQ) UNIV ROCKEFELLER.

XX PA (UYOR-) UNIV OREGON STATE.

XX PI Fischetti VA, Kruby DE;

XX DR WPI; 1991-022236/03.

XX DR N-PSDB; AAQ10244.

XX PT New recombinant streptococcal M protein DNA and viral vector - for
 PT production of poxviridae vaccines in treatment of vaccinia, fowlpox etc.

XX PS Disclosure; Fig 5; 41pp; English.

XX CC This M'6 protein corresponds to the conserved exposed polypeptide region
 CC of the streptococcal M protein. It is encoded by a gene- tically
 CC engineered gene introduced into the genome of a vaccinia or fowlpox
 CC virus. The resultant DNA complex is useful as a vaccine for
 CC immunoprotection against streptococcal infections. The M'6 polypeptide is
 CC the part of protein M responsible for virulence. (Updated on 25-MAR-2003
 CC to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 234 AA;

Query Match 52.6%; Score 72; DB 2; Length 234;
 Best Local Similarity 45.2%; Pred. No. 0.81;
 Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

QY 5 DKVK-----ASREAKQVEKALEOLEDKV 28
 Db 63 DKVKEEKQISDASRQLRRDLDSREAKQVEKALEANSKL 104

RESULT 14

AAR20128

ID AAR20128 standard; protein; 281 AA.

XX AC AAR20128;

XX DT 27-AUG-2003 (revised)

XX DT 15-APR-1992 (first entry)

XX DE Sequence encoded by truncated M1 gene.

XX KW Protein H; immunoglobulin G; IgG; antibody; autoimmune disease.

XX OS Streptococcus sp.

XX FH Key Location/Qualifiers

XX FT Region 1..28

XX FT Region /label= p16M1

XX FT Region 29..70

XX FT Region /label= C1

XX FT Region 71..112

XX FT Region /label= C2

XX FT Region 113..155

XX FT Region /label= C3

XX FT Region 156..176

XX FT Region /label= C4

XX FT Region 177..281

XX FT Region /label= D

XX PN WO9119740-A.

XX PD 26-DEC-1991.

XX PF 21-JUN-1990; 90SE-00002212.

XX PR 21-JUN-1990; 90SE-00002212.

XX PA (HIGH-) HIGHTECH RECEPTOR A.

XX PI Schmidt KH, Akesson P, Cooney J, Bjorck L;

XX DR WPI; 1992-024366/03.

XX DR N-PSDB; AAQ20292.

XX PT New IgG binding proteins H' lacking an albumin binding sequence - useful
 PT in purificn. of excess IgG from blood and to diagnose autoimmune
 PT diseases.

XX PS Disclosure; Fig 8; 37pp; English.

XX CC The inventors claim a protein prod. by a strain of Gp.A Streptococci. The
 CC protein has the AA sequence of protein H but lacks at least some part of
 CC the C and D regions (responsible for binding albumin), esp. it lacks the
 CC whole of these regions and extends for AA1 to AA158. Compared with
 CC natural protein H, it is more specific and may be used as part of a kit
 CC for the binding, separation and identification of human IgG. The same
 CC sequences appear in WO9119741. (Updated on 27-AUG-2003 to correct OS
 CC field.)

XX SQ Sequence 281 AA;

Query Match 52.6%; Score 72; DB 2; Length 281;
 Best Local Similarity 45.2%; Pred. No. 0.99;
 Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

QY 5 DKVK-----ASREAKQVEKALEOLEDKV 28
 Db 110 DKVKEEKQISDASRQLRRDLDSREAKQVEKALEANSKL 151

RESULT 15
AAP90955
ID AAP90955 standard; protein; 441 AA.
XX AC AAP90955;
XX DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 23-FEB-1990 (first entry)
XX DE M6 streptococcal protein.
XX KW Immunoglobulin.
XX OS Stretococcus sp; 'group A'.
XX FH Key Location/Qualifiers
FT Region 216. .235
FT Region 248. .269
FT Region 275. .284
XX PN W08909064-A.
XX PD 05-OCT-1989.
XX PF 13-MAR-1989; 89WO-US001026.
XX PR 25-MAR-1988; 88US-00173380.
PR 27-FEB-1989; 89US-00315588.
XX PA (UYRQ) UNIV ROCKEFELLER.
XX PI Fischetti VA;
XX WPI; 1989-309382/42.
XX PT Polypeptide(s) from streptococcal M protein - used to prepare vaccines
PT for providing protection against streptococcal infection.
XX PS Disclosure; Fig 1; 22pp; English.
XX CC The regions (pref. conjugated to a natural carrier, eg cholera toxin)
CC above can elicit an secretory Ig response in a mammal. They are used in
CC vaccines against streptococcal infection, and give protection to
CC different serotypes. (Updated on 25-MAR-2003 to correct PR field.)
CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to
CC correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)
XX SQ Sequence 441 AA;
Query Match 52.6%; Score 72; DB 1; Length 441;
Best Local Similarity 45.2%; Pred. No. 1.6;
Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;
QY 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
DB 270 DKVKEKQISDASRQGLRRDLASREAKKQVEKALEANSKL 311
Search completed: August 4, 2005, 08:59:24
Job time : 164.209 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2005, 08:27:17 ; Search time 40.4651 Seconds
(without alignments)
53.498 Million cell updates/sec

Title: US-10-706-275-2

Perfect score: 137

Sequence: 1 KOAEDKVKASREAKQVEKALEQLEDKVK 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/6C_COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	110	80.3	28	3	US-08-817-811-18
2	96	70.1	28	3	US-08-817-811-17
3	81	59.1	28	3	US-08-817-811-16
4	78	56.9	28	3	US-08-817-811-67
5	72	52.6	440	4	US-08-302-756B-35
6	72	52.6	443	2	US-08-795-475-6
7	72	52.6	443	4	US-08-325-278B-6
8	71	51.8	28	3	US-08-817-811-12
9	71	51.8	236	3	US-08-937-271-11
10	71	51.8	254	4	US-08-914-479A-4
11	71	51.8	284	4	US-08-914-479A-6
12	71	51.8	305	3	US-08-937-271-10
13	68.5	50.0	28	3	US-08-817-811-66
14	67	48.9	29	3	US-08-817-811-52
15	65.5	47.8	28	3	US-08-817-811-15
16	65	47.4	29	3	US-08-817-811-74
17	64	46.7	20	3	US-08-817-811-1
18	64	46.7	29	3	US-08-817-811-73
19	64	46.7	72	1	US-08-182-175A-87
20	64	46.7	72	5	PCT-US92-06412-87
21	64	46.7	361	4	US-09-543-681A-5390
22	63	46.0	29	3	US-08-817-811-79
23	63	46.0	107	1	US-08-182-175A-105
24	63	46.0	107	1	US-08-474-633A-92
25	63	46.0	107	4	US-08-823-771-92
26	63	46.0	107	5	PCT-US92-06412-105
27	62	45.3	28	3	US-08-817-811-13

28	45.3	29	3	US-08-817-811-78	Sequence 78, Appl
29	45.3	77	1	US-08-182-175A-57	Sequence 57, Appl
30	45.3	77	1	US-08-474-633A-75	Sequence 75, Appl
31	45.3	77	4	US-08-823-771-75	Sequence 75, Appl
32	45.3	77	5	PCT-US92-06412-57	Sequence 57, Appl
33	44.5	28	1	US-08-182-175A-49	Sequence 49, Appl
34	44.5	28	1	US-08-474-633A-58	Sequence 58, Appl
35	44.5	28	4	US-08-823-771-58	Sequence 49, Appl
36	44.5	28	5	PCT-US92-06412-49	Sequence 49, Appl
37	44.5	29	3	US-08-817-811-71	Sequence 71, Appl
38	44.5	29	3	US-08-817-811-72	Sequence 72, Appl
39	44.5	29	3	US-08-817-811-75	Sequence 75, Appl
40	44.5	29	3	US-08-817-811-89	Sequence 89, Appl
41	44.5	37	1	US-08-182-175A-85	Sequence 85, Appl
42	44.5	37	1	US-08-182-175A-97	Sequence 97, Appl
43	44.5	37	1	US-08-474-633A-85	Sequence 85, Appl
44	44.5	37	1	US-08-474-633A-86	Sequence 86, Appl
45	44.5	37	4	US-08-823-771-85	Sequence 85, Appl

ALIGNMENTS

RESULT 1
US-08-817-811-18
; Sequence 18, Application US/08817811
; Patent No. 6174528
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
; APPLICANT: Relif, Wendy A.
; APPLICANT: Good, Michael F.
; APPLICANT: Saul, Allan J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
; TITLE OF INVENTION: COMPRISING SAME
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,811
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 96/11944
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC:005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-817-811-18

Query Match 80.3%; Score 110; DB 3; Length 28;
Best Local Similarity 85.2%; Pred. No. 1.6e-06;
Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KOAEDKVKASREAKKQVEKALEQLEDK 27
 Db 2 KOAEDKVDASREAKKQVEKVKQLEDK 28

RESULT 2

US-08-817-811-17
 ; Sequence 17, Application US/08817811
 ; Patent No. 6174528
 ; GENERAL INFORMATION:
 ; APPLICANT: Cooper, Juan A.
 ; APPLICANT: Relf, Wendy A.
 ; APPLICANT: Good, Michael F.
 ; APPLICANT: Saul, Allan J.
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
 ; TITLE OF INVENTION: COMPRISING SAME
 ; NUMBER OF SEQUENCES: 97
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: USA
 ; ZIP: 77210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/817,811
 ; FILING DATE: 14-APR-1997
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO 96/11944
 ; FILING DATE: 25-APR-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Highlander, Steven L.
 ; REGISTRATION NUMBER: 37,642
 ; REFERENCE/DOCKET NUMBER: FBRC:005
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 512/418-3000
 ; TELEFAX: 512/474-7577
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 28 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-08-817-811-17

Query Match 70.1%; Score 96; DB 3; Length 28;
 Best Local Similarity 76.9%; Pred. NO. 6.4e-05;
 Matches 20; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KOAEDKVKASREAKKQVEKALEQLED 26
 Db 3 KOAEDKLDASREAKKQVEDKVKQLED 28

RESULT 3

US-08-817-811-16
 ; Sequence 16, Application US/08817811
 ; Patent No. 6174528
 ; GENERAL INFORMATION:
 ; APPLICANT: Cooper, Juan A.
 ; APPLICANT: Relf, Wendy A.
 ; APPLICANT: Good, Michael F.
 ; APPLICANT: Saul, Allan J.
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
 ; TITLE OF INVENTION: COMPRISING SAME
 ; NUMBER OF SEQUENCES: 97
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: USA
 ; ZIP: 77210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/817,811
 ; FILING DATE: 14-APR-1997
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO 96/11944
 ; FILING DATE: 25-APR-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Highlander, Steven L.
 ; REGISTRATION NUMBER: 37,642
 ; REFERENCE/DOCKET NUMBER: FBRC:005
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 512/418-3000
 ; TELEFAX: 512/474-7577
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 28 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-08-817-811-16

Query Match 59.1%; Score 81; DB 3; Length 28;
 Best Local Similarity 68.0%; Pred. NO. 0.0035;
 Matches 17; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 KOAEDKVKASREAKKQVEKALEQLE 25
 Db 4 KOAEDLDASREAKKQVDKVKQLE 28

RESULT 4

US-08-817-811-67
 ; Sequence 67, Application US/08817811
 ; Patent No. 6174528
 ; GENERAL INFORMATION:
 ; APPLICANT: Cooper, Juan A.
 ; APPLICANT: Relf, Wendy A.
 ; APPLICANT: Good, Michael F.
 ; APPLICANT: Saul, Allan J.
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
 ; TITLE OF INVENTION: COMPRISING SAME
 ; NUMBER OF SEQUENCES: 97
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: USA
 ; ZIP: 77210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/817,811
 ; FILING DATE: 14-APR-1997
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO 96/11944
 ; FILING DATE: 25-APR-1996

US-08-817-811-67
 ; Sequence 67, Application US/08817811
 ; Patent No. 6174528
 ; GENERAL INFORMATION:
 ; APPLICANT: Cooper, Juan A.
 ; APPLICANT: Relf, Wendy A.
 ; APPLICANT: Good, Michael F.
 ; APPLICANT: Saul, Allan J.
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
 ; TITLE OF INVENTION: COMPRISING SAME
 ; NUMBER OF SEQUENCES: 97
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: USA
 ; ZIP: 77210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/817,811
 ; FILING DATE: 14-APR-1997
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO 96/11944
 ; FILING DATE: 25-APR-1996

```
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Highlander, Steven L.
/ REGISTRATION NUMBER: 37,642
/ REFERENCE/DOCKET NUMBER: FBRC:005
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512/418-3000
/ TELEFAX: 512/474-7577
/ INFORMATION FOR SEQ ID NO: 67:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/
US-08-817-811-67

Query Match 56.9%; Score 78; DB 3; Length 28;
Best Local Similarity 64.0%; Pred. No. 0.0077;
Matches 16; Conservative 5; Mismatches 0; Gaps 0;

QY 1 KQAEQKVKASREAKKQVEKALEQLE 25
      |||| : ||||| : : |||
Db 4 KQAEDDLDSREAKKQLQDKVKQLE 28

RESULT 5
US-08-302-756E-35
/ Sequence 35, Application US/08302756E
/ Patent No. 6737521
/ GENERAL INFORMATION:
/ APPLICANT: FISCHETTI, Vincent A.
/ APPLICANT: POZZI, Gianni
/ APPLICANT: SCHNEEWIND, Olaf
/ TITLE OF INVENTION: DELIVERY AND EXPRESSION OF A HYBRID SURFACE PROTEIN ON
/ TITLE OF INVENTION: THE SURFACE OF GRAM POSITIVE BACTERIA
/ FILE REFERENCE: 016921-076
/ CURRENT APPLICATION NUMBER: US/08/302,756E
/ CURRENT FILING DATE: 1995-03-07
/ PRIOR APPLICATION NUMBER: US 07/522,440
/ PRIOR FILING DATE: 1990-05-11
/ PRIOR APPLICATION NUMBER: US 07/742,199
/ PRIOR FILING DATE: 1991-08-05
/ PRIOR APPLICATION NUMBER: US 07/814,823
/ PRIOR FILING DATE: 1991-12-23
/ PRIOR APPLICATION NUMBER: US 07/851,082
/ PRIOR FILING DATE: 1992-03-13
/ PRIOR APPLICATION NUMBER: PCT/US93/02355
/ PRIOR FILING DATE: 1993-03-12
/ NUMBER OF SEQ ID NOS: 61
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 35
/ TYPE: PRT
/ LENGTH: 440
/ ORGANISM: S. pyogenes
/
US-08-302-756E-35

Query Match 52.6%; Score 72; DB 4; Length 440;
Best Local Similarity 45.2%; Pred. No. 0.64;
Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

QY 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
      |||| |
Db 270 DKVKEKQISDASRQLRRDLDSREAKKQVEKALEANSKL 311

RESULT 6
US-08-795-475-6
/ Sequence 6, Application US/08795475
/ Patent No. 5965390
/ GENERAL INFORMATION:
/ APPLICANT: Bjvrck, Lars
/ APPLICANT: Sjobring, Ulf
/ TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
/ NUMBER OF SEQUENCES: 14
```

```
/ CORRESPONDENCE ADDRESS:
/ ADDRESSES: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/795,475
/ FILING DATE: 11-FEB-1997
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mcmasters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 100084.402D1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 443 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
US-08-795-475-6

Query Match 52.6%; Score 72; DB 2; Length 443;
Best Local Similarity 45.2%; Pred. No. 0.65;
Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

QY 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
      |||| |
Db 272 DKVKEKQISDASRQLRRDLDSREAKKQVEKALEANSKL 313

RESULT 7
US-08-325-278B-6
/ Sequence 6, Application US/08325278B
/ Patent No. 6822075
/ GENERAL INFORMATION:
/ APPLICANT: Bjorck, Lars
/ APPLICANT: Sjobring, Ulf
/ TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
/ NUMBER OF SEQUENCES: 15
/ CORRESPONDENCE ADDRESS:
/ ADDRESSES: Seed IP Law Group
/ STREET: 701 Fifth Avenue Suite 6300
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/325,278B
/ FILING DATE: 26-Oct-1994
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Potter, Jane E. R.
/ REGISTRATION NUMBER: 33,332
/ REFERENCE/DOCKET NUMBER: 100084.402
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 6:
```

```

; SEQUENCE CHARACTERISTICS:
;   LENGTH: 443 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-325-278B-6

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```

Query Match      52.6%; Score 72; DB 4; Length 443;
Best Local Similarity 45.2%; Pred. No. 0.65;
Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

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QY      5 DKVK-----ASREAKQVEKALEQLEDKV 28
DB      272 DKVKEKQISDASRQLRRLLDASREAKQVEKALEEANSKL 313

```

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RESULT 8
US-08-817-811-12
; Sequence 12, Application US/08817811
; Patent No. 6174528
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
; APPLICANT: Relif, Wendy A.
; APPLICANT: Good, Michael F.
; APPLICANT: Saul, Allan J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
; TITLE OF INVENTION: COMPRISING SAME
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,811
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 96/11944
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC:005
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 28 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
US-08-817-811-12

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Query Match      51.8%; Score 71; DB 3; Length 28;
Best Local Similarity 55.6%; Pred. No. 0.049;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

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QY      1 KQAEKVKASREAKQVEKALEQLEDK 27
DB      2 KQLEDKVKQLEDKVKQLEDKV 28

```

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RESULT 9

```

```

US-08-937-271-11
; Sequence 11, Application US/08937271
; Patent No. 6063386
; GENERAL INFORMATION:
; APPLICANT: Dale, James B.
; APPLICANT: Lederer, James W.
; TITLE OF INVENTION: RECOMBINANT MULTIVALENT M PROTEIN
; TITLE OF INVENTION: VACCINE
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,271
; FILING DATE: 15-SEP-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenman, Stephen J.
; REGISTRATION NUMBER: 43,058
; REFERENCE/DOCKET NUMBER: 481112.405C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 236 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-937-271-11

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Query Match      51.8%; Score 71; DB 3; Length 236;
Best Local Similarity 75.0%; Pred. No. 0.44;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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QY      9 ASREAKQVEKALEQLEDKV 28
DB      87 ASREAKQVEKALEEANSKL 106

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RESULT 10
US-08-914-479A-4
; Sequence 4, Application US/08914479A
; Patent No. 6419932
; GENERAL INFORMATION:
; APPLICANT: Dale, James B.
; TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
; TITLE OF INVENTION: FOR GROUP A STREPTOCOCCAL VACCINE
; FILE REFERENCE: 481112.404C2
; CURRENT APPLICATION NUMBER: US/08/914,479A
; CURRENT FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 08/409,270
; PRIOR FILING DATE: 1995-03-23
; PRIOR APPLICATION NUMBER: 07/945,860
; PRIOR FILING DATE: 1992-09-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: An antigen of M5 and a carrier of the
; COOH-terminal portion of M5
US-08-914-479A-4

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ATTORNEY/AGENT INFORMATION:

Query Match 50.0%; Score 68.5; DB 3; Length 28;
Best Local Similarity 55.2%; Pred. No. 0.096;
Matches 16; Conservative 4; Mismatches 2; Indels

Qy 1 KOAEDKVKASREAKQVEKALEQLEDKVK 29
Db 4 KOAEDKV-----KQEDKVEELQDKVK 25

RESULT 14
US-08-817-811-52
; Sequence 52, Application US/08817811
; Patent No. 6174528
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
; APPLICANT: Relf, Wendy A.
; APPLICANT: Good, Michael F.
; APPLICANT: Saul, Allan J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,811
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 96/11944
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC:005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-817-811-52
Query Match 48.9%; Score 67; DB 3; Length 29;
Best Local Similarity 48.3%; Pred. No. 0.15;
Matches 14; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
Qy 1 KOAEDKVKASREAKQVEKALEQLEDKVK 29
Db 1 KQEDKVVMAQPTADRLTEKLNQLEDKVK 29
RESULT 15
US-08-817-811-15
; Sequence 15, Application US/08817811
; Patent No. 6174528
; GENERAL INFORMATION:
; APPLICANT: Cooper, Juan A.
; APPLICANT: Relf, Wendy A.
; APPLICANT: Good, Michael F.
; APPLICANT: Saul, Allan J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,811
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 96/11944
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC:005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-817-811-15
Query Match 47.8%; Score 65.5; DB 3; Length 28;
Best Local Similarity 58.6%; Pred. No. 0.21;
Matches 17; Conservative 2; Mismatches 3; Indels 7; Gaps 1;
Qy 1 KOAEDKVKASREAKQVEKALEQLEDKVK 29
Db 5 KOAERDLDSREAKK-----QLQDKVK 26
Search completed: August 4, 2005, 08:38:31
Job time : 40.4651 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2005, 08:36:38 ; Search time 141.628 Seconds
(without alignments)
. 79.939 Million cell updates/sec

Title: US-10-706-275-2

Perfect score: 137

Sequence: 1 KQAEKVKASREAKQVEKALEQLEDKVK 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1752860 segs, 390397842 residues

Total number of hits satisfying chosen parameters: 1752860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	137	100.0	29	17 US-10-706-275-2	Sequence 2, Appli
2	137	100.0	29	17 US-10-706-275-15	Sequence 15, Appl
3	125	91.2	28	17 US-10-706-275-13	Sequence 12, Appl
4	119	86.9	28	17 US-10-706-275-12	Sequence 13, Appl
5	112	81.8	28	17 US-10-706-275-14	Sequence 14, Appl
6	110	80.3	28	17 US-10-706-275-11	Sequence 11, Appl
7	96	70.1	28	17 US-10-706-275-10	Sequence 10, Appl
8	81	59.1	28	17 US-10-706-275-9	Sequence 9, Appli
9	72	52.6	443	8 US-08-325-278-6	Sequence 6, Appli
10	72	52.6	553	16 US-10-474-792-672	Sequence 672, App
11	72	52.6	558	17 US-10-732-923-3295	Sequence 3295, App

12	71	51.8	254	13	US-10-141-627-4	Sequence 4, Appli
13	71	51.8	284	13	US-10-141-627-6	Sequence 6, Appli
14	67	48.9	389	15	US-10-282-122A-67145	Sequence 67145, A
15	65.5	47.8	28	17	US-10-706-275-8	Sequence 8, Appli
16	64	46.7	14	17	US-10-706-275-1	Sequence 1, Appli
17	64	46.7	20	13	US-10-044-034-22	Sequence 22, Appl
18	64	46.7	20	17	US-10-706-275-5	Sequence 5, Appli
19	63	46.0	107	14	US-10-023-066A-92	Sequence 92, Appl
20	63	46.0	107	17	US-10-804-678-92	Sequence 92, Appl
21	62	45.3	28	17	US-10-706-275-6	Sequence 6, Appli
22	62	45.3	77	14	US-10-023-066A-75	Sequence 75, Appl
23	62	45.3	77	17	US-10-804-678-75	Sequence 75, Appl
24	61	44.5	28	14	US-10-023-066A-58	Sequence 58, Appl
25	61	44.5	28	17	US-10-804-678-58	Sequence 58, Appl
26	61	44.5	37	14	US-10-023-066A-85	Sequence 85, Appl
27	61	44.5	37	14	US-10-023-066A-86	Sequence 86, Appl
28	61	44.5	37	17	US-10-804-678-85	Sequence 85, Appl
29	61	44.5	37	17	US-10-804-678-86	Sequence 86, Appl
30	61	44.5	56	14	US-10-023-066A-77	Sequence 77, Appl
31	61	44.5	56	17	US-10-804-678-77	Sequence 77, Appl
32	61	44.5	145	16	US-10-437-963-146357	Sequence 146357,
33	61	44.5	145	16	US-10-437-963-146368	Sequence 146368,
34	60	43.8	35	14	US-10-023-066A-62	Sequence 62, Appl
35	60	43.8	35	17	US-10-804-678-62	Sequence 62, Appl
36	60	43.8	42	14	US-10-023-066A-34	Sequence 34, Appl
37	60	43.8	42	17	US-10-804-678-34	Sequence 34, Appl
38	60	43.8	49	14	US-10-023-066A-30	Sequence 30, Appl
39	60	43.8	49	14	US-10-023-066A-32	Sequence 32, Appl
40	60	43.8	49	14	US-10-023-066A-54	Sequence 54, Appl
41	60	43.8	49	17	US-10-804-678-30	Sequence 30, Appl
42	60	43.8	49	17	US-10-804-678-32	Sequence 32, Appl
43	60	43.8	49	17	US-10-804-678-54	Sequence 54, Appl
44	60	43.8	56	14	US-10-023-066A-79	Sequence 79, Appl
45	60	43.8	56	17	US-10-804-678-79	Sequence 79, Appl

ALIGNMENTS

RESULT 1
US-10-706-275-2
; Sequence 2, Application US/10706275
; Publication No. US20050002956A1
; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec
; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.
; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.
; APPLICANT: Good, Michael F.
; APPLICANT: Batzloff, Michael R.
; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10/706,275
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide derivative of S. pyogenes with flanking sequen
; OTHER INFORMATION: es
US-10-706-275-2

Query Match 100.0%; Score 137; DB 17; Length 29;
Best Local Similarity 100.0%; Pred. No. 7.8e-09;

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Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKAEKVKASREAKKQVEKALEQLEDKVK 29
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Db 1 QKAEKVKASREAKKQVEKALEQLEDKVK 29

RESULT 2
US-10-706-275-15
; Sequence 15, Application US/10706275
; Publication No. US20050002956A1
; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec
; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.
; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.
; APPLICANT: Good, Michael F.
; APPLICANT: Batzloff, Michael R.
; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10/706,275
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-15

Query Match 100.0%; Score 137; DB 17; Length 29;
Best Local Similarity 100.0%; Pred. No. 7.8e-09;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKAEKVKASREAKKQVEKALEQLEDKVK 29
    |||||
Db 1 QKAEKVKASREAKKQVEKALEQLEDKVK 29

RESULT 3
US-10-706-275-12
; Sequence 12, Application US/10706275
; Publication No. US20050002956A1
; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec
; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.
; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.
; APPLICANT: Good, Michael F.
; APPLICANT: Batzloff, Michael R.
; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10/706,275
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-12

Query Match 100.0%; Score 137; DB 17; Length 29;
Best Local Similarity 100.0%; Pred. No. 7.8e-09;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QKAEKVKASREAKKQVEKALEQLEDKVK 29

RESULT 4
US-10-706-275-13
; Sequence 13, Application US/10706275
; Publication No. US20050002956A1
; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec
; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.
; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.
; APPLICANT: Good, Michael F.
; APPLICANT: Batzloff, Michael R.
; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10/706,275
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-13

Query Match 86.9%; Score 119; DB 17; Length 28;
Best Local Similarity 89.3%; Pred. No. 8.3e-07;
Matches 25; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QKAEKVKASREAKKQVEKALEQLEDKVK 29
    |||||
Db 1 QKAEKVKASREAKKQVEKALEQLEDKVK 28

RESULT 5
US-10-706-275-14
; Sequence 14, Application US/10706275
; Publication No. US20050002956A1
; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec
; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.
; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.
; APPLICANT: Good, Michael F.
; APPLICANT: Batzloff, Michael R.
; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10/706,275
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-14

Query Match 86.9%; Score 119; DB 17; Length 28;
Best Local Similarity 89.3%; Pred. No. 8.3e-07;
Matches 25; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QKAEKVKASREAKKQVEKALEQLEDKVK 29
    |||||
Db 1 QKAEKVKASREAKKQVEKALEQLEDKVK 28

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-12

Query Match 91.2%; Score 125; DB 17; Length 28;
Best Local Similarity 92.9%; Pred. No. 1.7e-07;
Matches 26; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKAEKVKASREAKKQVEKALEQLEDKVK 28
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Db 1 QKAEKVKASREAKKQVEKALEQLEDKVK 28

RESULT 4
US-10-706-275-13
; Sequence 13, Application US/10706275
; Publication No. US20050002956A1
; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec
; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.
; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.
; APPLICANT: Good, Michael F.
; APPLICANT: Batzloff, Michael R.
; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10/706,275
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-13

Query Match 86.9%; Score 119; DB 17; Length 28;
Best Local Similarity 89.3%; Pred. No. 8.3e-07;
Matches 25; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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    |||||
Db 1 QKAEKVKASREAKKQVEKALEQLEDKVK 28

RESULT 5
US-10-706-275-14
; Sequence 14, Application US/10706275
; Publication No. US20050002956A1
; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec
; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.
; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.
; APPLICANT: Good, Michael F.
; APPLICANT: Batzloff, Michael R.
; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10/706,275
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-14

Query Match 86.9%; Score 119; DB 17; Length 28;
Best Local Similarity 89.3%; Pred. No. 8.3e-07;
Matches 25; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QKAEKVKASREAKKQVEKALEQLEDKVK 29
    |||||
Db 1 QKAEKVKASREAKKQVEKALEQLEDKVK 28

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; PRIOR APPLICATION NUMBER: AU 2002302132
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-14

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Query Match      81.8%; Score 112; DB 17; Length 28;
Best Local Similarity 88.9%; Pred. No. 5.2e-06;
Matches 24; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 3 ASDKVKASREAKKQVEKALEQLEDKVK 29
Db 1 ASDKVKQLREAKKQVEKALEQLEDKVKQ 27

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RESULT 6
US-10-706-275-11
; Sequence 11, Application US/10706275
; Publication No. US20050002956A1
; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec
; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.
; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.
; APPLICANT: Good, Michael F.
; APPLICANT: Batzloff, Michael R.
; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10/706,275
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-11

```

```

Query Match      80.3%; Score 110; DB 17; Length 28;
Best Local Similarity 85.2%; Pred. No. 8.7e-06;
Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 KOAEDKVKASREAKKQVEKALEQLEDK 27
Db 2 KOAEDKVDASREAKKQVEKKVKQLEDK 28

```

```

RESULT 7
US-10-706-275-10
; Sequence 10, Application US/10706275
; Publication No. US20050002956A1
; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec
; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.
; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.
; APPLICANT: Good, Michael F.
; APPLICANT: Batzloff, Michael R.

```

```

; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10/706,275
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-10

```

```

Query Match      70.1%; Score 96; DB 17; Length 28;
Best Local Similarity 76.9%; Pred. No. 0.00034;
Matches 20; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 KOAEDKVKASREAKKQVEKALEQLED 26
Db 3 KOAEDKLDASREAKKQVEDKVKQLED 28

```

```

RESULT 8
US-10-706-275-9
; Sequence 9, Application US/10706275
; Publication No. US20050002956A1
; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec
; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.
; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.
; APPLICANT: Good, Michael F.
; APPLICANT: Batzloff, Michael R.
; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10/706,275
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-9

```

```

Query Match      59.1%; Score 81; DB 17; Length 28;
Best Local Similarity 68.0%; Pred. No. 0.017;
Matches 17; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 1 KOAEDKVKASREAKKQVEKALEQLE 25
Db 4 KOAEDDLASREAKKQVQDKVKQLE 28

```

```

RESULT 9
US-08-325-278-6
; Sequence 6, Application US/08325278
; Publication No. US20030027283A1
; GENERAL INFORMATION:

```

APPLICANT: Bjvrck, Lars
 APPLICANT: Sjvbring, Ulf
 TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/325,278
 FILING DATE: 26-OCT-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: McMasters, David D.
 REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 450023.401
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 443 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-325-278-6

```

Query Match      52.6%; Score 72; DB 8; Length 443;
Best Local Similarity 45.2%; Pred.No. 3.4;
Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

QY 5 DRVK-----ASREAKQVKEALEQEDKV 28
    |||||
DB 272 DKYEEKQISDASRQRLRRDLDSREAKQVKEALEANSKL 313
    |||||

```

```

RESULT 10
US-10-474-792-672
; Sequence 672, Application US/10474792
; Publication No. US20040236072A1
; GENERAL INFORMATION:
; APPLICANT: Olmsted, Stephen
; APPLICANT: Zagursky, Robert
; APPLICANT: Nickbarg, Elliot
; APPLICANT: Winter, Lourie
; TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
; FILE REFERENCE: AM 100359
; CURRENT APPLICATION NUMBER: US/10/474,792
; CURRENT FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 672
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-474-792-672

```

```

Query Match      52.6%; Score 72; DB 16; Length 553;
Best Local Similarity 45.2%; Pred. No. 4.3;
Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

QY 5 DKVK-----ASREAKQVKEALEQLEDKV 28
Db 382 DKYKEEKQISDASRGUURRLDLSREAKQVKEALEEANSKI 423

```

```

RESULT 11
US-10-732-923-3295
; Sequence 3295, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15 (52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 3295
; LENGTH: 558
; TYPE: PR1
; ORGANISM: Streptococcus pyogenes
US-10-732-923-3295

```

```

Query Match      52.8%; Score 72; DB 17; Length 558;
Best Local Similarity 50.0%; Pred. No. 4.3;
Matches 18; Conservative 3; Mismatches 7; Indels 8; Gaps 1;

Qy 1 KQAE-----KVKASREAKQVKEKALEQLEDKV 28
Db 393 KQTSASRQGLRDLDASREAKQVKEKALEEANSKL 428

```

```

RESULT 12
US-10-141-627-4
; Sequence 4, Application US/10141627
; Publication No. US20020176863A1
; GENERAL INFORMATION:
; APPLICANT: Dale, James B.
; TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
; TITLE OF INVENTION: FOR GROUP A STREPTOCOCCAL VACCINE
; FILE REFERENCE: 481112.404C3
; CURRENT APPLICATION NUMBER: US/10/141,627
; CURRENT FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: An antigen of M5 and a carrier of the
; OTHER INFORMATION: COOH-terminal portion of M5
US-10-141-627-4

```

```

Query Match      51.8%; Score 71; DB 13; Length 254;
Best Local Similarity 75.0%; Pred. No. 2.4;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      9 ASREAAKQVEKALEQLEQKV 28
        |||||
Db      105 ASREAAKQVEKALEEANSKL 124

```

```

RESULT 13
US-10-141-627-6
; Sequence 6, Application US/10141627
; Publication No. US20020176863A1
; GENERAL INFORMATION:
; APPLICANT: Dale, James B.
; TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
; TITLE OF INVENTION: FOR GROUP A STREPTOCOCCAL VACCINE
; FILE REFERENCE: 481112.404C3
; CURRENT APPLICATION NUMBER: US/10/141,627
; CURRENT FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0

```

```
; SEQ ID NO 6
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: An antigen of three fragments of M5 and a carrier
; OTHER INFORMATION: of the COOH-terminal portion of M5
US-10-141-627-6

Query Match          51.8%; Score 71; DB 13; Length 284;
Best Local Similarity 75.0%; Pred. No. 2.8;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 9 ASREAKKQVEKALEQLEDKV 28
Db 135 ASREAKKQVEKALEANSKL 154

RESULT 14
US-10-282-122A-67145
; Sequence 67145, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Cart, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67145
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-10-282-122A-67145

Query Match          48.9%; Score 67; DB 15; Length 389;
Best Local Similarity 51.6%; Pred. No. 11;
Matches 16; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

QY 1 KOAED--KVKASREAKKQVEKALEQLEDKVK 29

; SEQ ID NO 6
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: An antigen of three fragments of M5 and a carrier
; OTHER INFORMATION: of the COOH-terminal portion of M5
US-10-141-627-6

Query Match          51.8%; Score 71; DB 13; Length 284;
Best Local Similarity 75.0%; Pred. No. 2.8;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 9 ASREAKKQVEKALEQLEDKV 28
Db 135 ASREAKKQVEKALEANSKL 154

RESULT 15
US-10-706-275-8
; Sequence 8, Application US/10706275
; Publication No. US20050002956A1
; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec
; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.
; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.
; APPLICANT: Good, Michael F.
; APPLICANT: Batzloff, Michael R.
; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10/706,275
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-8

Query Match          47.8%; Score 65.5; DB 17; Length 28;
Best Local Similarity 58.6%; Pred. No. 0.99;
Matches 17; Conservative 2; Mismatches 3; Indels 7; Gaps 1;

QY 1 KOAEDKVKASREAKKQVEKALEQLEDKVK 29
Db 5 KOAERDLDSREAKK-----QLQDKVK 26

Search completed: August 4, 2005, 08:55:14
Job time : 142.628 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2005, 08:50:19 ; Search time 31.6977 Seconds
(without alignments)
88.028 Million cell updates/sec

Title: US-10-706-275-2

Perfect score: 137

Sequence: 1 KOAEDVKASREAKQVEKALEQLEDKVK 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72.5	52.9	587	2 JCI1419	Fc gamma (IgG) rec
2	72	52.6	388	2 A49545	plasmaenogen-bindin
3	72	52.6	408	2 S30283	protein M precursor
4	72	52.6	436	2 S30284	M protein precursor
5	72	52.6	454	2 S43556	plasmaenogen-bindin
6	72	52.6	472	2 S43554	plasmaenogen-bindin
7	72	52.6	483	2 A26297	M6 protein - Strept
8	72	52.6	484	2 S35401	M1 protein precursor
9	72	52.6	484	2 S46489	M1 protein precursor
10	72	52.6	484	2 S34978	M1.i protein precursor
11	72	52.6	501	2 A44643	M protein precursor
12	72	52.6	532	2 S54871	M protein - Strept
13	72	52.6	564	2 A60115	M protein precursor
14	71	51.8	492	2 A28616	M5 protein precursor
15	71	51.8	539	2 A28549	M24 protein precursor
16	70	51.1	528	2 S57835	IgG-binding protei
17	66	48.2	1365	2 T45031	hypothetical prote
18	66	48.2	1408	2 T45039	hypothetical prote
19	64	46.7	217	2 G75219	hypothetical prote
20	63.5	46.4	104	1 H64327	conserved hypothet
21	62	45.3	493	2 T22180	hypothetical prote
22	61	44.5	445	2 T50972	probable zootin [i
23	60	43.8	284	2 S23470	beta-tropomyosin -
24	60	43.8	876	2 AF0843	alanine-tRNA ligas
25	59	43.1	284	1 TMRBB	tropomyosin beta c
26	59	43.1	284	1 TMRP1	tropomyosin 1, emb
27	59	43.1	284	2 A23562	tropomyosin 1, fib
28	59	43.1	284	2 S00922	tropomyosin beta,
29	59	43.1	284	2 A44131	tropomyosin beta 2

30	59	43.1	284	2 S03838	tropomyosin beta,
31	59	43.1	284	2 S23256	tropomyosin beta -
32	59	43.1	284	2 B25073	tropomyosin beta,
33	59	43.1	436	2 AHI387	cell wall binding
34	58	42.3	217	2 B71203	hypothetical prote
35	58	42.3	284	1 TMCHS1	tropomyosin 1, amo
36	58	42.3	284	2 A30125	tropomyosin 1, ske
37	58	42.3	751	2 T34490	hypothetical prote
38	58	42.3	2116	2 A26655	myosin heavy chain
39	57.5	42.0	558	2 D70449	conserved hypothet
40	57	41.6	169	2 E97357	hypothetical prote
41	57	41.6	174	2 A12174	general stress pro
42	57	41.6	248	2 A25530	tropomyosin, fibro
43	57	41.6	248	2 S11390	tropomyosin 5 - mo
44	57	41.6	248	2 S34124	tropomyosin isofor
45	57	41.6	248	2 I53784	tropomyosin - rat

ALIGNMENTS

RESULT 1

JCI1419 Fc gamma (IgG) receptor II precursor - Streptococcus sp.

N:Alternate names: fcrv protein

C:Species: Streptococcus sp.

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: JCI1419; S17354

R:Smirnov, O.Y.; Denesnyuk, A.I.; Zakharov, M.V.; Abramov, V.M.; Zav'yalov, V.P.

Gene 120, 27-32, 1992

A:Title: Protein V, a novel type-II Igg receptor from Streptococcus sp.: Sequence, homol

A:Reference number: JCI1419; MUID:93013016; PMID:1398120

A:Accession: JCI1419

A:Molecule type: DNA

A:Residues: 1-587 <SMI>

A:Cross-references: UNIPROT:Q55312; EMBL:X62467; NID:g47562; PIDN:CAA44324.1; PID:g4756

A:Experimental source: strain 22/58'Valente'

C:Genetics:

A:Gene: fcrv

C:Superfamily: M5 protein

C:Keywords: duplication; immunoglobulin receptor

F:1-41/Domain: signal sequence #status predicted <SIG>

F:42-587/Product: Igg Fc receptor II #status predicted <MAT>

F:234-268/Region: 35-residue repeat A

F:269-303/Region: 35-residue repeat A

F:304-338/Region: 35-residue repeat A

F:339-373/Region: 35-residue repeat A

F:374-408/Region: 35-residue repeat B

F:416-450/Region: 35-residue repeat B

Query Match 52.9%; Score 72.5; DB 2; Length 587;

Best Local Similarity 46.3%; Pred. No. 2.5;

Matches 19; Conservative 3; Mismatches 6; Indels 13; Gaps 1;

QY 1 KOAEDK-----VKASREAKQVEKALEQLEDKVK 28

Db 417 KVKEKQKISDSRQGLRRDLDSREAKQVEKALEANSKL 457

RESULT 2

A49545

plasmaenogen-binding protein PAM precursor - Streptococcus pyogenes (fragment)

N:Alternate names: plasmaenogen-binding M-like protein (Pd 53)

C:Species: Streptococcus pyogenes

C>Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004

C:Accession: A49545; S61084; S60829; S70459; S32619

R:Berge, A.; Sjoeborg, U.

J. Biol. Chem. 268, 25417-25424, 1993

A:Title: PAM, a novel plasmaenogen-binding protein from Streptococcus pyogenes.

A:Reference number: A49545; MUID:94064605; PMID:8244975

A:Accession: A49545

A:Molecule type: DNA

A:Residues: 1-388 <BER>


```

RESULT 6
S43554
M6 protein - Streptococcus sp. (fragment)
C:Species: Streptococcus sp.
A:Variety: group G
C>Date: 07-Sep-1994 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000
C:Accession: S45599; S43554
R:Ben Naar, A.; Wistedt, A.; Ringdahl, U.; Sjoeborg, U.
Eur. J. Biochem. 222, 267-276, 1994
A:Title: Streptokinase activates plasminogen bound to human group C and G streptococci
A:Reference number: S45598; MUID:94291620; PMID:8020466
A:Accession: S45599
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-472 <BE2>
A:CROSS-references: EMBL:Z32678; NID:9474769; PIDN:CAA83589.1; PID:g1333838
C:Superfamily: M5 protein

Query Match 52.6%; Score 72; DB 2; Length 472;
Best Local Similarity 45.2%; Pred. No. 2.3;
Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

QY 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
DB 328 DKVKEKQISDTSRKGRLRRDLDSREAKKQVEKALEEANSKL 369

RESULT 7
A26297
M6 protein - Streptococcus pyogenes
C:Species: Streptococcus pyogenes
C>Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
C:Accession: A26297
R:Hollingshead, S.K.; Fischetti, V.A.; Scott, J.R.
J. Biol. Chem. 261, 1677-1686, 1986
A:Title: Complete nucleotide sequence of type 6 M protein of the group A streptococcus.
A:Reference number: A26297; MUID:8611835; PMID:3511046
A:Accession: A26297
A:Molecule type: DNA
A:Residues: 1-483 <HOL>
A:CROSS-references: UNIPROT:P08089; GB:M11338; GB:M11415; NID:g153699; PIDN:AAA26920.1;
C:Genetics: emm6
C:Superfamily: M5 protein
C:Keywords: coiled coil; transmembrane protein

Query Match 52.6%; Score 72; DB 2; Length 483;
Best Local Similarity 45.2%; Pred. No. 2.4;
Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

QY 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
DB 312 DKVKEKQISDASRQGLRRDLDSREAKKQVEKALEEANSKL 353

RESULT 8
S35401
M1 protein precursor - Streptococcus pyogenes
C:Species: Streptococcus pyogenes
A:Variety: serotype M1
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: S35401; S61074; S60784
R:Podbielski, A.
submitted to the EMBL Data Library, September 1991
A:Reference number: S35401
A:Accession: S35401
A:Molecule type: DNA
A:Residues: 1-484 <PDB>
A:CROSS-references: UNIPROT:Q10372; EMBL:X62131; NID:g311757; PIDN:CAA44062.1; PID:g3117
R:Whitmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
submitted to the EMBL Data Library, July 1994
A:Description: Noncongruent relationships between variation in emm1 gene sequences and p

```

```

A:Reference number: S61072
A:Accession: S61074
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 16-94 <WHA>
A:CROSS-references: EMBL:U11940; NID:G533557; PIDN:AAA99556.1; PID:G533558
R:Whitmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
A:Title: Non-congruent relationships between variation in emm gene sequences and the po
A:Reference number: S60784; MUID:95198537; PMID:7891551
A:Accession: S60784
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 29-89 <WH2>
A:CROSS-references: EMBL:U11940
C:Genetics: emm1
C:Superfamily: M5 protein

Query Match 52.6%; Score 72; DB 2; Length 484;
Best Local Similarity 45.2%; Pred. No. 2.4;
Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

QY 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
DB 313 DKVKEKQISDASRQGLRRDLDSREAKKQVEKALEEANSKL 354

RESULT 9
S46489
M1 protein precursor - Streptococcus pyogenes
C:Species: Streptococcus pyogenes
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S46489; S46490
R:Akesson, P.; Schmidt, K.H.; Cooney, J.; Bjoerck, L.
Biochem. J. 300, 877-886, 1994
A:Title: M1 protein and protein H: IgGFC- and albumin-binding streptococcal surface prot
A:Reference number: S46489; MUID:94280417; PMID:8010973
A:Accession: S46489
A:Molecule type: DNA
A:Residues: 1-484 <AKS>
A:CROSS-references: UNIPROT:Q05464; UNIPROT:Q10372; UNIPROT:Q99XV0
A:Experimental source: strain 40/58, serotype M1
A:Accession: S46490
A:Molecule type: protein
A:Residues: 42-51 <AKW>
A:Experimental source: strain 40/58, serotype M1
C:Genetics: emm1
C:Superfamily: M5 protein
C:Keywords: transmembrane protein
F1-41/Domain: signal sequence #status predicted <SIG>
F142-484/Product: M1 protein #status experimental <NAT>
F1459-477/Domain: transmembrane #status predicted <TMM>

Query Match 52.6%; Score 72; DB 2; Length 484;
Best Local Similarity 45.2%; Pred. No. 2.4;
Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

QY 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
DB 313 DKVKEKQISDASRQGLRRDLDSREAKKQVEKALEEANSKL 354

RESULT 10
S34978
M1.1 protein precursor - Streptococcus pyogenes
C:Species: Streptococcus pyogenes
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: S34978; S31966
R:Harbaugh, M.P.; Podbielski, A.; Huegl, S.; Cleary, P.P.
Mol. Microbiol. 8, 981-991, 1993
A:Title: Nucleotide substitutions and small-scale insertion produce size and antigenic v

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A:Reference number: S34978; MUID:93360826; PMID:8355619
 A:Accession: S34978
 A:Molecule type: DNA
 A:Residues: 1-484 <HAR>
 A:Cross-references: UNIPROT:Q05464; EMBL:Z21845; NID:G49401; PIDN:CAA79893.1; PID:G49402
 C:Genetics:
 A:Gene: emm1.1
 C:Superfamily: M5 protein
 C:Keywords: membrane protein
 F:1-42/Domain: signal sequence #status predicted <SIG>
 F:43-484/Product: M1.1 protein #status predicted <MAT>

Query Match 52.6%; Score 72; DB 2; Length 484;
 Best Local Similarity 45.2%; Pred. No. 2.4;
 Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

Oy 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
 |||||
 Db 313 DKVKEKQISDASRQGLRRDLDSREAKKQVEKALEANSKL 354

RESULT 11

A44643
 M protein precursor - Streptococcus pyogenes (serotype M57) (fragment)
 C:Species: Streptococcus pyogenes
 A:Variety: serotype M57
 C:Date: 26-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 10-Dec-1999
 C:Accession: A44643; S60833
 R:Manjula, B.N.; Khandke, K.M.; Fairwell, T.; Relf, W.A.; Sriprakash, K.S.
 J. Protein Chem. 10, 369-384, 1991
 A:Title: Heptad motifs within the distal subdomain of the coiled-coil rod region of M protein: nucleotide sequence of the M57 gene and relation of the deduced
 A:Reference number: A44643; MUID:92143933; PMID:1781883

A:Accession: A44643
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-501 <MAN>
 A:Experimental source: type M57, strain A395
 A:Note: sequence inconsistent with nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBIN:83737, NCBIIP:83738)
 A:Note: parts of this sequence were confirmed by peptide sequencing
 R:Whitmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
 Mol. Microbiol. 14, 619-631, 1994
 A:Title: Non-congruent relationships between variation in emm gene sequences and the population
 A:Reference number: S60784; MUID:95198537; PMID:7891551
 A:Accession: S60833

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 14-95 <WHA>

A:Cross-references: EMBL:U11971
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
 C:Superfamily: M5 protein
 C:Keywords: coiled coil; dimer

Query Match 52.6%; Score 72; DB 2; Length 501;
 Best Local Similarity 45.2%; Pred. No. 2.4;
 Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

Oy 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
 |||||
 Db 342 DKVKEKQISDASRQGLRRDLDSREAKKQVEKALEANSKL 383

RESULT 12

S54871
 M protein - Streptococcus sp.
 C:Species: Streptococcus sp.
 C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
 C:Accession: S54871
 R:Podolski, A.; Melzer, B.
 submitted to the EMBL Data Library, June 1991
 A:Reference number: S54871
 A:Accession: S54871

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-532 <POD>
 A:Cross-references: UNIPROT:Q55098; EMBL:X60097; NID:G840905; PIDN:CAA42693.1; PID:G8409
 C:Superfamily: M5 protein

Query Match 52.6%; Score 72; DB 2; Length 532;
 Best Local Similarity 45.2%; Pred. No. 2.6;
 Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

Oy 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
 |||||
 Db 361 DKVKEKQISDASRQGLRRDLDSREAKKQVEKALEANSKL 402

RESULT 13

A60115
 M protein precursor - Streptococcus pyogenes (serotype M12) (fragment)
 C:Species: Streptococcus pyogenes
 A:Variety: serotype M12
 C:Date: 08-Dec-1992 #sequence_revision 08-Dec-1992 #text_change 09-Jul-2004
 C:Accession: A40174; A60115; S39887; S61072; S60793
 R:Robbins, J.C.; Spanier, J.G.; Jones, S.J.; Simpson, W.J.; Cleary, P.P.
 J. Bacteriol. 169, 5633-5640, 1987
 A:Title: Streptococcus pyogenes type 12 M protein gene regulation by upstream sequences.
 A:Reference number: A40174; MUID:88058777; PMID:2445730
 A:Accession: A40174
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-564 <ROB>
 A:Cross-references: UNIPROT:P19401; GB:M18269; NID:G153543; PIDN:AAA88573.1; PID:G153544
 R:Kraus, W.; Seyer, J.M.; Beachey, E.H.
 Infect. Immun. 57, 2457-2461, 1989
 A:Title: Vimentin-cross-reactive epitope of type 12 streptococcal M protein.
 A:Reference number: A60115; MUID:89307564; PMID:2473037
 A:Accession: A60115
 A:Molecule type: protein
 A:Residues: 42-54 <KXA>
 R:Chen, C.; Bormann, N.; Cleary, P.P.
 Mol. Gen. Genet. 241, 685-693, 1993
 A:Title: VirR and Mry are homologous trans-acting regulators of M protein and Csa peptidase
 A:Reference number: S39886; MUID:94088463; PMID:7505389
 A:Accession: S39887

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-15 <CHE>
 R:Whitmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
 submitted to the EMBL Data Library, July 1994
 A:Description: Noncongruent relationships between variation in emm gene sequences and the population
 A:Reference number: S61072
 A:Accession: S61072
 A:Molecule type: DNA
 A:Residues: 13-111 <WHA>

A:Cross-references: EMBL:U11937; NID:G533551; PIDN:AAA99553.1; PID:G1235807
 R:Whitmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
 Mol. Microbiol. 14, 619-631, 1994
 A:Title: Non-congruent relationships between variation in emm gene sequences and the population
 A:Reference number: S60784; MUID:95198537; PMID:7891551
 A:Accession: S60793

A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 29-89 <WHW>
 A:Cross-references: EMBL:U11937
 C:Genetics:
 A:Gene: emm12
 C:Superfamily: M5 protein

C:Keywords: transmembrane protein
 F:1-41/Domain: signal sequence #status predicted <SIG>
 F:42-564/Product: M protein (fragment) #status predicted <MAT>

Query Match 52.6%; Score 72; DB 2; Length 564;
 Best Local Similarity 45.2%; Pred. No. 2.7;
 Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 ASREAKKQVEKALEQLEDKV 28
 |||||
 Db 390 ASREAKKQVEKALEEANSKL 409

Search completed: August 4, 2005, 09:04:11
 Job time : 32.6977 secs

Qy 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
 |||||
 Db 405 DKVKEEQISDASRQGLRDLDSREAKKQVEKALEEANSKL 446

RESULT 14

A28616

M5 protein precursor - Streptococcus pyogenes

C:Species: Streptococcus pyogenes

A:Variety: serotype M5

C:Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 09-Jul-2004

C:Accession: A28616; S60787

R:Miller, L.; Gray, L.; Beachey, E.; Kehoe, M.

J. Biol. Chem. 263, 5668-5673, 1988

A:Title: Antigenic variation among group A streptococcal M proteins. Nucleotide sequence

A:Reference number: A28616; MUID:88186881; PMID:3281944

A:Accession: A28616

A:Molecule type: DNA

A:Residues: 1-492 <MIL>

A:Cross-references: UNIPROT:P02977; GB:M20374; NID:g153812; PIDN:AAA26976.1; PID:g153813

R:Whitmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.

Mol. Microbiol. 14, 619-631, 1994

A:Title: Non-congruent relationships between variation in emm gene sequences and the pop

A:Reference number: S60784; MUID:95198537; PMID:7891551

A:Accession: S60787

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A:Molecule type: DNA

A:Residues: 30-89 <WHA>

C:Genetics:

A:Gene: smps

C:Superfamily: M5 protein

C:Keywords: coiled coil; transmembrane protein

F:1-42/Domain: signal sequence #status predicted <SIG>

F:43-492/Product: M5 protein #status predicted <MAT>

Query Match 51.8%; Score 71; DB 2; Length 492;
 Best Local Similarity 75.0%; Pred. No. 3;
 Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 ASREAKKQVEKALEQLEDKV 28
 |||||
 Db 343 ASREAKKQVEKALEEANSKL 362

RESULT 15

A28549

M24 protein precursor - Streptococcus pyogenes

C:Species: Streptococcus pyogenes

A:Variety: serotype M24

C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004

C:Accession: A28549; S60802

R:Mouw, A.R.; Beachey, E.H.; Burdett, V.

J. Bacteriol. 170, 676-684, 1988

A:Title: Molecular evolution of streptococcal M protein: cloning and nucleotide sequence

A:Reference number: A28549; MUID:88115166; PMID:3276665

A:Accession: A28549

A:Molecule type: DNA

A:Residues: 1-539 <MOU>

A:Cross-references: UNIPROT:P12379; GB:M19031; NID:g153616; PIDN:AAA26874.1; PID:g153617

R:Whitmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.

Mol. Microbiol. 14, 619-631, 1994

A:Title: Non-congruent relationships between variation in emm gene sequences and the pop

A:Reference number: S60784; MUID:95198537; PMID:7891551

A:Accession: S60802

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A:Molecule type: DNA

A:Residues: 30-89 <WHA>

C:Superfamily: M5 protein

C:Keywords: coiled coil; transmembrane protein

Query Match 51.8%; Score 71; DB 2; Length 539;
 Best Local Similarity 75.0%; Pred. No. 3.3;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2005, 08:38:38 ; Search time 153.767 Seconds
(without alignments)
96.576 Million cell updates/sec

Title: US-10-706-275-2
Perfect score: 137
Sequence: 1 KQAEKVKASREAKKQVEKALEQLEDKVK 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74.5	54.4	592	2 Q00720	Q00720 streptococc
2	72.5	52.9	454	2 Q840T7	Q840T7 streptococc
3	72.5	52.9	550	2 Q54840	Q54840 streptococc
4	72.5	52.9	587	2 Q55312	Q55312 streptococc
5	72	52.6	100	2 Q54639	Q54639 streptococc
6	72	52.6	100	2 Q54640	Q54640 streptococc
7	72	52.6	100	2 Q9R3A1	Q9R3A1 streptococc
8	72	52.6	198	2 Q54832	Q54832 streptococc
9	72	52.6	208	2 P95824	P95824 streptococc
10	72	52.6	208	2 P95826	P95826 streptococc
11	72	52.6	237	2 Q5TLR5	Q6CLR5 streptococc
12	72	52.6	251	2 Q6V9Q3	Q6V9Q3 streptococc
13	72	52.6	279	2 Q8GL87	Q8GL87 streptococc
14	72	52.6	282	2 Q8GLA6	Q8GLA6 streptococc
15	72	52.6	303	2 Q8GL98	Q8GL98 streptococc
16	72	52.6	307	2 Q8GL84	Q8GL84 streptococc
17	72	52.6	314	2 Q8GLB0	Q8GLB0 streptococc
18	72	52.6	317	2 Q8GL92	Q8GL92 streptococc
19	72	52.6	319	2 Q8GLA2	Q8GLA2 streptococc
20	72	52.6	322	2 Q8GLA4	Q8GLA4 streptococc
21	72	52.6	326	2 Q8GL91	Q8GL91 streptococc
22	72	52.6	340	2 Q8GLA1	Q8GLA1 streptococc
23	72	52.6	369	2 Q8GL90	Q8GL90 streptococc
24	72	52.6	388	1 PAM_STRPY	P49054 streptococc
25	72	52.6	400	2 Q8NZ79	Q8NZ79 streptococc
26	72	52.6	408	2 Q54837	Q54837 streptococc
27	72	52.6	435	2 Q9AMM3	Q9AMM3 streptococc
28	72	52.6	436	2 Q54839	Q54839 streptococc
29	72	52.6	441	2 Q55246	Q55246 streptococc
30	72	52.6	443	2 Q54703	Q54703 streptococc
31	72	52.6	454	2 Q55278	Q55278 streptococc

32	72	52.6	465	2 Q83XW0	Q83XW0 streptococc
33	72	52.6	472	2 Q55279	Q55279 streptococc
34	72	52.6	483	1 M6_STRPY	P08089 streptococc
35	72	52.6	484	2 Q05464	Q05464 streptococc
36	72	52.6	484	2 Q10372	Q10372 streptococc
37	72	52.6	484	2 Q99XV0	Q99XV0 streptococc
38	72	52.6	488	2 Q54830	Q54830 streptococc
39	72	52.6	500	2 Q9RHV2	Q9RHV2 streptococc
40	72	52.6	508	2 Q76MJ2	Q76MJ2 streptococc
41	72	52.6	532	2 Q55098	Q55098 streptococc
42	72	52.6	558	2 Q54718	Q54718 streptococc
43	72	52.6	564	1 M12_STRPY	P19401 streptococc
44	72	52.6	581	2 Q54835	Q54835 streptococc
45	72	52.6	581	2 Q8K5P9	Q8K5P9 streptococc

ALIGNMENTS

RESULT 1
Q00720 PRELIMINARY; PRT; 592 AA.
AC Q00720;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE M protein precursor.
OS Streptococcus sp. (Lancefield group G).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1320;
RN [1]
RC STRAIN=1750;
RX MEDLINE=92363566; PubMed=1500178;
RA Collins C.M., Kimura A., Bisno A.L.;
RT "Group G streptococcal M protein exhibits structural features
analogous to class I M protein of group A streptococci.";
RL Infect. Immun. 60:3689-3696(1992).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
DR EMBL; M95774; AAA26928.1; -;
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR011000; ApoLP_III like.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF02370; M; 2.
DR Pfam; PF04650; YsIRK signal; 1.
DR PRINTS; PR00015; GPOSANCHOR.
DR TIGRFAMs; TIGR01167; LPXTG anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 41 Potential.
FT CHAIN 42 592 M protein.
SQ SEQUENCE 592 AA; 67008 MW; 821399D030DE5CEB CRC64;

Query Match 54.4%; Score 74.5; DB 2; Length 592;
Best Local Similarity 46.3%; Pred. No. 16;
Matches 19; Conservative 4; Mismatches 5; Indels 13; Gaps 1;

Qy 1 KQAEK-----VKASREAKKQVEKALEQLEDKV 28
Db 422 KVKEDKQISDASRKGLRRDLKASREAKKQVEKALEEANSKL 462

RESULT 2
Q840T7 PRELIMINARY; PRT; 454 AA.
ID Q840T7

AC Q840T7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE M protein (Fragment).
GN Name=emm;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RA Dyall-Smith M.L., Sripakash K.S.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY263387; AA092603.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF02370; M; 1.
FT NON_TER 1 454
FT NON_TER 454 454
SQ SEQUENCE 454 AA; 51368 MW; 4DF100DAA6467864 CRC64;

Query Match 52.9%; Score 72.5; DB 2; Length 454;
Best Local Similarity 46.3%; Pred. No. 20;
Matches 19; Conservative 3; Mismatches 6; Indels 13; Gaps 1;

Qy 1 KQAEK-----VKASREAKKQVEKALEQLEDKV 28
| | | : ||||| :
Db 381 KVKEDKQISDASRQGLRRDLDSREAKKQVEKALEANSKL 421

RESULT 3
Q54840
ID Q54840 PRELIMINARY; PRT; 550 AA.
AC Q54840;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE M protein.
GN Name=emm5;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=serotype M55;
RL MEDLINE=95371690; PubMed=7643859; DOI=10.1016/0161-5890(95)00022-7;
RA Boyle M.D.P., Weber-Heynenann J., Raeder R., Podbielski A.;
RT "Characterization of a gene coding for a type Ito bacterial IgG-binding protein.";
RL Mol. Immunol. 32:669-678(1995).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
DR EMBL; X72090; CAA50980.1; -;
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR005877; Gpos_Ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF00746; Gram_pos_anchor.
DR Pfam; PF02370; M; 2.
DR Pfam; PF04650; Ysirk signal; 1.
DR PRINTS; PR00015; GPOSANCHOR.
DR TIGRFAMs; TIGR01167; LPXTG anchor; 1.
DR TIGRFAMs; TIGR01168; Ysirk signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall, Peptidoglycan-anchored.
SQ SEQUENCE 550 AA; 61736 MW; 32894BFF9805181B CRC64;

Query Match 52.9%; Score 72.5; DB 2; Length 550;
Best Local Similarity 46.3%; Pred. No. 24;
Matches 19; Conservative 3; Mismatches 6; Indels 13; Gaps 1;

Qy 1 KQAEK-----VKASREAKKQVEKALEQLEDKV 28
| | | : ||||| :
Db 381 KVKEDKQISDASRQGLRRDLDSREAKKQVEKALEANSKL 421

RESULT 4
Q55312
ID Q55312 PRELIMINARY; PRT; 587 AA.
AC Q55312;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Protein V precursor.
GN Name=fcrV;
OS Streptococcus sp.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1306;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Valente;
RL MEDLINE=93013016; PubMed=1398120; DOI=10.1016/0378-1119(92)90005-A;
RA Smirnov O.Y., Denesjuk A.I., Zakharov M.V., Abramov V.M.,
Zav'yalov V.P.;
RT "Protein V, a novel type-II IgG receptor from Streptococcus sp.: sequence, homologues and putative Fc-binding site.";
RL Gene 120:27-32(1992).
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).
DR EMBL; X62467; CAA44324.1; -;
DR PIR; JCI419; JCI419.
DR HSP; O15813; ID7M.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR005877; Gpos_Ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF02370; M; 1.
DR Pfam; PF04650; Ysirk signal; 1.
DR PRINTS; PR00015; GPOSANCHOR.
DR TIGRFAMs; TIGR01167; LPXTG anchor; 1.
DR TIGRFAMs; TIGR01168; Ysirk signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall, Peptidoglycan-anchored; Signal.
FT SIGNAL 1 44 potential.
FT CHAIN 45 587 protein V.
SQ SEQUENCE 587 AA; 64130 MW; D9FA5658AC23FA81 CRC64;

Query Match 52.9%; Score 72.5; DB 2; Length 587;
Best Local Similarity 46.3%; Pred. No. 25;
Matches 19; Conservative 3; Mismatches 6; Indels 13; Gaps 1;

Qy 1 KQAEK-----VKASREAKKQVEKALEQLEDKV 28
| | | : ||||| :
Db 417 KVKEDKQISDASRQGLRRDLDSREAKKQVEKALEANSKL 457

RESULT 5
Q54639
ID Q54639 PRELIMINARY; PRT; 100 AA.
AC Q54639;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE M1 protein (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]

```
RP SEQUENCE FROM N.A.
RX MEDLINE=9517252; PubMed=7868273; Pan X., Swanson D.S., Martin D.R.;
RA Musser J.M., Kapur V., Szeto J., Pan X., Swanson D.S., Martin D.R.;
RT "Genetic diversity and relationships among Streptococcus pyogenes
RT strains expressing serotype M1 protein: recent intercontinental spread
RT of a subclone causing episodes of invasive disease.";
RL Infect. Immun. 63:994-1003(1995).
DR EMBL; U20103; AAA85116.1; -.
DR HSSP; P13276; IEQ1.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF02370; M; 1.
FT NON_TER 1
FT NON_TER 100
SQ SEQUENCE 100 AA; 11243 MW; 9775831FA25DC463 CRC64;

Query Match 52.6%; Score 72; DB 2; Length 100;
Best Local Similarity 45.2%; Pred. No. 5.9;
Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

QY 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
DB 28 DKVKEKQISDASRQGLRRDLASREAKKQVEKALEANSKL 69

RESULT 6
Q54640 ID Q54640 PRELIMINARY; PRT; 100 AA.
AC Q54640;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE M1 protein (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9517252; PubMed=7868273;
RA Musser J.M., Kapur V., Szeto J., Pan X., Swanson D.S., Martin D.R.;
RT "Genetic diversity and relationships among Streptococcus pyogenes
RT strains expressing serotype M1 protein: recent intercontinental spread
RT of a subclone causing episodes of invasive disease.";
RL Infect. Immun. 63:994-1003(1995).
DR EMBL; U20104; AAA85117.1; -.
DR HSSP; P13276; IEQ1.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF02370; M; 1.
FT NON_TER 1
FT NON_TER 100
SQ SEQUENCE 100 AA; 11287 MW; 9773331914EDC2D3 CRC64;

Query Match 52.6%; Score 72; DB 2; Length 100;
Best Local Similarity 45.2%; Pred. No. 5.9;
Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

QY 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
DB 28 DKVKEKQISDASRQGLRRDLASREAKKQVEKALEANSKL 69

RESULT 7
Q9R3A1 ID Q9R3A1 PRELIMINARY; PRT; 100 AA.
AC Q9R3A1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE M1 protein (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9517252; PubMed=7868273;
RA Musser J.M., Kapur V., Szeto J., Pan X., Swanson D.S., Martin D.R.;
RT "Genetic diversity and relationships among Streptococcus pyogenes
RT strains expressing serotype M1 protein: recent intercontinental spread
RT of a subclone causing episodes of invasive disease.";
RL Infect. Immun. 63:994-1003(1995).
DR EMBL; U20102; AAA85115.1; -.
DR EMBL; U20101; AAA85114.1; -.
DR HSSP; P13276; IEQ1.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF02370; M; 1.
FT NON_TER 1
FT NON_TER 100
SQ SEQUENCE 100 AA; 11345 MW; 9773331C00EDC2D3 CRC64;

Query Match 52.6%; Score 72; DB 2; Length 100;
Best Local Similarity 45.2%; Pred. No. 5.9;
Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

QY 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
DB 28 DKVKEKQISDASRQGLRRDLASREAKKQVEKALEANSKL 69

RESULT 8
Q54832 ID Q54832 PRELIMINARY; PRT; 198 AA.
AC Q54832;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE M protein (Fragment).
GN Name=emm3;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3-3/317;
RX MEDLINE=93062420; PubMed=1435517;
RA Podbielski A., Baird R., Kaufhold A.;
RT "The group A streptococcal M-type 3 protein gene exhibits a C terminus
RT typical for class I M proteins.";
RL Med. Microbiol. Immunol. 181:209-213(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=3-3/317;
RA Podbielski A., Kaufhold A.;
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; X66816; CAA47295.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR003345; M_repeat_anchor.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF02370; M; 1.
DR PRINTS; PR00015; GP0SANCHOR.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
FT NON_TER 1
FT NON_TER 198
SQ SEQUENCE 198 AA; 21550 MW; A738888D947155D5 CRC64;

Query Match 52.6%; Score 72; DB 2; Length 198;
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Best Local Similarity 45.2%; Pred. No. 11;
Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

QY 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
   |||||
Db 27 DKVKEKQISDASRQGLRDLDSREAKKQVEKALEEANSKL 68

RESULT 9
P95824 ID P95824 PRELIMINARY; PRT; 208 AA.
AC P95824;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE M protein (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M nontypeable group A;
RA Brandt E.R., Good M.F.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; U65899; AAB40640.1; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF02370; M; 1.
DR PRINTS; PR00015; GPANCHOR.
DR TIGRFAMs; TIGR01167; LPXTG anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall, Peptidoglycan-anchor.
FT NON_TER 1
FT NON_TER 208
SQ SEQUENCE 208 AA; 22695 MW; 013FBBAB0A97FF42 CRC64;

Query Match 52.6%; Score 72; DB 2; Length 208;
Best Local Similarity 45.2%; Pred. No. 11;
Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

QY 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
   |||||
Db 37 DKVKEKQISDASRQGLRDLDSREAKKQVEKALEEANSKL 78

RESULT 10
P95826 ID P95826 PRELIMINARY; PRT; 208 AA.
AC P95826;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE M protein (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RHD152-;
RA Brandt E.R., Good M.F.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; U66005; AAB40642.1; -.
DR GO; GO:0009986; C:cell surface; IEA.

Query Match 52.6%; Score 72; DB 2; Length 208;
Best Local Similarity 45.2%; Pred. No. 11;
Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

QY 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
   |||||
Db 37 DKVKEKQISDASRQGLRDLDSREAKKQVEKALEEANSKL 78

RESULT 11
Q6TLR5 ID Q6TLR5 PRELIMINARY; PRT; 237 AA.
AC Q6TLR5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE M protein (Fragment).
GN Name=emm;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NS241;
RX MEDLINE=22894607; PubMed=14532198;
RA Moses A.E., Hidalgo-Grass C., Dan-Goor M., Jaffe J., Shetzigovsky I.,
RA Ravins M., Koreman Z., Cohen-Poradosu R., Nir-Paz R.;
RT "emm typing of M nontypeable invasive group A streptococcal isolates
RT in Israel.";
RL J. Clin. Microbiol. 41:4655-4659(2003).
DR EMBL; AY394538; AAQ94530.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF02370; M; 1.
FT NON_TER 1
FT NON_TER 237
SQ SEQUENCE 237 AA; 27027 MW; 47CFF315DD4EB5F2 CRC64;

Query Match 52.6%; Score 72; DB 2; Length 237;
Best Local Similarity 42.5%; Pred. No. 13;
Matches 17; Conservative 6; Mismatches 5; Indels 12; Gaps 1;

QY 1 KOAEDKVK-----ASREAKKQVEKALEQLEDKV 28
   |:::|
Db 172 KEQNKI5EASRKGLRDLDSREAKKQVEKALEEANSKL 211

RESULT 12
Q6V9Q3 ID Q6V9Q3 PRELIMINARY; PRT; 251 AA.
AC Q6V9Q3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE M protein (Fragment).
GN Name=emm;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF02370; M; 1.
DR PRINTS; PR00015; GPANCHOR.
DR TIGRFAMs; TIGR01167; LPXTG anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall, Peptidoglycan-anchor.
FT NON_TER 1
FT NON_TER 208
SQ SEQUENCE 208 AA; 22565 MW; 79972A987324729B CRC64;

Query Match 52.6%; Score 72; DB 2; Length 208;
Best Local Similarity 45.2%; Pred. No. 11;
Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

QY 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
   |||||
Db 37 DKVKEKQISDASRQGLRDLDSREAKKQVEKALEEANSKL 78

RESULT 11
Q6TLR5 ID Q6TLR5 PRELIMINARY; PRT; 237 AA.
AC Q6TLR5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE M protein (Fragment).
GN Name=emm;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NS241;
RX MEDLINE=22894607; PubMed=14532198;
RA Moses A.E., Hidalgo-Grass C., Dan-Goor M., Jaffe J., Shetzigovsky I.,
RA Ravins M., Koreman Z., Cohen-Poradosu R., Nir-Paz R.;
RT "emm typing of M nontypeable invasive group A streptococcal isolates
RT in Israel.";
RL J. Clin. Microbiol. 41:4655-4659(2003).
DR EMBL; AY394538; AAQ94530.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF02370; M; 1.
FT NON_TER 1
FT NON_TER 237
SQ SEQUENCE 237 AA; 27027 MW; 47CFF315DD4EB5F2 CRC64;

Query Match 52.6%; Score 72; DB 2; Length 237;
Best Local Similarity 42.5%; Pred. No. 13;
Matches 17; Conservative 6; Mismatches 5; Indels 12; Gaps 1;

QY 1 KOAEDKVK-----ASREAKKQVEKALEQLEDKV 28
   |:::|
Db 172 KEQNKI5EASRKGLRDLDSREAKKQVEKALEEANSKL 211

RESULT 12
Q6V9Q3 ID Q6V9Q3 PRELIMINARY; PRT; 251 AA.
AC Q6V9Q3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE M protein (Fragment).
GN Name=emm;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J58;
RA Moses A.B., Hidalgo-Grass C., Dan-Goor M., Jaffe J., Shtzigovsky I.,
RA Ravina M., Korenman Z., Cohen-Poradosu R., Nir-Paz R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY346386; AAQ73206.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF02370; M; 1.
FT NON_TER 1
FT NON_TER 251
SQ SEQUENCE 251 AA; 28938 MW; 2A66602AAA637D11 CRC64;

Query Match 52.6%; Score 72; DB 2; Length 251;
Best Local Similarity 45.2%; Pred. No. 13;
Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

QY 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
    |||||
DB 199 DKVKEKQISDSRQGLRRDLASREAKKQVEKALEANSKL 240
    |||||

RESULT 13
Q8GL87
ID O8GL87 PRELIMINARY; PRT; 279 AA.
AC O8GL87;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE M protein (Fragment).
GN Name=emm;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RA Dyall-Smith M.L., Krejany S., Sriprakash K.S., Delvecchio A.,
RA McMillan D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY139420; AAN64693.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF02370; M; 2.
FT NON_TER 1
FT NON_TER 279
SQ SEQUENCE 279 AA; 31224 MW; 16A600455BC5C3A0 CRC64;

Query Match 52.6%; Score 72; DB 2; Length 279;
Best Local Similarity 45.2%; Pred. No. 15;
Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

QY 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
    |||||
DB 202 DKVKEKQISDSRQGLRRDLASREAKKQVEKALEANSKL 243
    |||||

RESULT 14
Q8GLA6
ID O8GLA6 PRELIMINARY; PRT; 282 AA.
AC O8GLA6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE M protein (Fragment).
GN Name=emm;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
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RN [1]
RP SEQUENCE FROM N.A.
RA Dyall-Smith M.L., Krejany S., Sriprakash K.S., Delvecchio A.,
RA McMillan D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY139401; AAN64674.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF02370; M; 1.
FT NON_TER 1
FT NON_TER 282
SQ SEQUENCE 282 AA; 32157 MW; 5C799B0AA4323541 CRC64;

Query Match 52.6%; Score 72; DB 2; Length 282;
Best Local Similarity 45.2%; Pred. No. 15;
Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

QY 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
    |||||
DB 204 DKVKEKQISDSRQGLRRDLASREAKKQVEKALEANSKL 245
    |||||

RESULT 15
Q8GL98
ID O8GL98 PRELIMINARY; PRT; 303 AA.
AC O8GL98;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE M protein (fragment).
GN Name=emm;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RA Dyall-Smith M.L., Krejany S., Sriprakash K.S., Delvecchio A.,
RA McMillan D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY139409; AAN64682.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003345; M_repeat.
DR Pfam; PF02370; M; 2.
FT NON_TER 1
FT NON_TER 303
SQ SEQUENCE 303 AA; 34562 MW; F76F37540E16CD1B CRC64;

Query Match 52.6%; Score 72; DB 2; Length 303;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 18; Conservative 3; Mismatches 7; Indels 8; Gaps 1;

QY 1 KQAE-----KVKSREAKKQVEKALEQLEDKV 28
    |||||
DB 230 KQVSDASRQGLRRDLASREAKKQVEKALEANSKL 265
    |||||

Search completed: August 4, 2005, 09:03:17
Job time : 153.767 secs
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